

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGTCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCATCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGA¹CTGCCCAGCGCCCCAGG
CTGGACTGAGCCCCCTACGCCCCCTGCAGCCCCCATGCCCTGCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTTTTCTCCTC
CCCTTCCCTCGGGAGGGTCCCAGACCCTGGCATGGGATGGGCTGGGATTTT²TTTGTGAAT
CCACCCCTGGCTACCCCCACCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAA
CGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVAGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCVPGKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

0978255-104504

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
GTCAGCCCACGGCGGGGACTATGGTGAAATTTCCGGCGCTCAGCACTACTGGCCCCGTGATC
CGGTTCTTGGTGCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGTTT
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGCCAGGGGCCATCGC
TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTGTGC
TTCACAGTCACCTGGAATGCCGGGAGCCCTGCTCATCCGATCCTCTCCTTGTACATGGGC
GCACCTGTGCGCTGCACCACCTGTGCTGGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTG
ACAAGAATAACCCAGCAACAACTGGTGAGCAGGCAACACAGTCACGGCAGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCCAGTCACAGTGAGGGCGCAT
CTCACGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGCCCCAGCTCTGTGCTGCG
GATCATCGTCCTCATCGCCAGCCTCGTGGTCTTACCCTACCTGGGGGTGCACGGTGCAGCCC
TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG
TGCTATGTCTACCGGAAGCAGAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
CTCTGCCATGACAGACATGCCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG
AGAATGAATAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
GGCATCATCTCTCCCTCTCCCATCGTATTTTGTTCCTTTTGTGTTTGTGTTTGGTAAT
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC
TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC
TCCTCCCTGGACAATCTCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
CACCCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
TTAAAACTCGGCTTCTTTGATTTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
GAGGCGGGTGGCAGCTGCAGCCCGGAGTCCCCGTTCACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG
GGCAGCAAACCTGACATGGTTGAATGATAGCATTTCCTCTGCGTTCTCCTAGATCTGAGCAA
GCTGTGAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTAAATTGTCAAAAA
GCGCATCTCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC
CTTTCCTGAAGGTGCGATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT
TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA
TTGAGAATGTACTACGGTACTTCCCTCCACACCATAACGATAAAGCAAGACATTTTATAACG
ATACCAGAGTCACTATGTGGTCTCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA
TATTTTTCTAAGTTTTGGAAAGCAGGTTTTTCTTTTAAAAAAATTTATAGACACGGTTCACT
AAATTGATTTAGTCAGAAATCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCGC
ATTTTCAATAAAATGTCTCTAATACAAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSDFKNVGLVFNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIINKLHHVDESV
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCGLYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR
IFSFFPVVPTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGvHGATLGvGSLL
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMDMPPTTEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

0907265 101501

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG
ACAAGAATAACCCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

097225.1050
FBI - 5623/560

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTINTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTGCGGATTTTCT
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

030225.1054
105401.56282680

FIGURE 7

TATTTCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCCTACCTGGGGGTGCACGGTGAGAC

09078295.101501

104-10181

GCCCGCCGCGCGCGCCGGGGCGCCCGAAGCCCGGGAGCCACCGCCATGGGGGGCTGCCTGGGA
 GCCTGCTCCCTGCTCAGCTGCGCGTCTTGCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
 CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTTCCTCTTCC
 TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGAGAGTACAGCTCTACAAGCTG
 CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCTTGCCAGGGCCACATCGACTGTGG
 CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
 TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
 AATGGGTTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
 CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGTTGGGCTCCTTCCTCTTCA
 TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
 AAGGCCGAGGAGTGCATTCCTGCGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT
 CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCCAGCGGCT
 GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
 GCTGTCTTGCCCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT
 CACCTCTACACCATGTTTTGTCACTGGTCAAGCCCTATCCAGTATCCCTGAACAGAAATGCA
 ACCCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
 ACCCAGTGGTGGGATGCCCCGAGCATTTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT
 CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCAGGAGTGCC
 CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC
 TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT
 GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
 TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
 TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT
 CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
 GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG
 CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
 GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCCTCCTCCTGT
 TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCCTCAGGCTCCACGGGAGCGGGG
 CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
 CCTGGTCACGTCCCCCAGGGGACCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT
 AAGACTTTTTTCTAATAAACAAGCCAGTGCGTGTAAAAAAA

FIGURE 9

MGACLGACSLLSCLSCSCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGLVLSIIMLSPGVE
SOLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLFILIQLVLLIDFAHSW
NQRWLKGABECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYTTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVTSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

09572205.101501

FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG
TGA CTGCCGATT CGGAAGT CCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCCTTAAGCCATTTTGTAATTGCAGGA
GCTGTACGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTT CAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC
CTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTCTT
TTTA ACTAAGAATGGGGCTGTTG TACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTGCAAAAAGATTAAAGTTGAATTTTACAGTTT

097325.10501

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQVIEQSQAETIYHNRFDVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDLSHFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

09473295.101501

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG
GCTGGCGCCGAACC

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LAND OFFICE
OF THE STATE OF NEW YORK
FOR THE YEAR 1901

FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

097225.101504

FIGURE 14

GAGCCGCCGCCGCGCGCGCGCGCGCACTGCAGCCCCAGGCCCGGCCCGCCACCCACGTCT
 GCGTTGCTGCCCCGCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT
 CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCAGGG
 GCTTCGCGTGTTCGAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGTTAGTCTG
 CTGCTAATTGGAATTGCTGCGTGGGGCATTTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
 CGGCGTGGTCATTCAGTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
 CTGTAAAACATCATCAGGTGTTTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTTATT
 GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
 GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
 GTGGGTTCCGAAGTGTTAACCCTAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC
 TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
 TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
 GGAACCAGAAAGACCCCCGCGCAATCCTAGTGCAATCCTTTGATGAGAAAACAAGGAAGAT
 TTCCTTCGTATTATGATCTTGTTCACCTTCTGTAATTTCTGTTAAGCTCCATTTGCCAGT
 TTAAGGAAGGAAACACTATCTGGAAGAGTACCTTATTGATAGTGAATTATATATTTTTACT
 CTATGTTTCTCTACATGTTTTTTCTTTCCGTTGCTGAAAAATATTTGAACTTGTGGTCTC
 TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCAATGTGCGGCACTGTCCACTGTGGCCTT
 TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA
 TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCCTAC
 TGGAAAAAGAGTGGAATTTATTAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
 TCCAAATCCCAATTTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
 TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
 GTCTTAGGAAATGTGGTTTAAATTTTGAATTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT
 CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
 TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
 AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG
 ATTATCTTAAAAATTGTTAAATACCGTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT
 GTCAAACCTAAGCATATTTGAATATGATCTCCCATATTTGAAATTGAAATCGTATTGTGTG
 GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA
 ATTAAAAGAAAGTAATGGAAG

105101-5628660

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

092325.104504
T09401.56232660

FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCTGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

09478295.101501

FIGURE 17

AATCCCAAATTCCCAATTTTTTTGGNCTTTTATAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTGTACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

09978295.101501

FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCACTTTTATGGTATCTTGCGCTTGTTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

09078295-101501

SECRET

SECRET

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGV LWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPPEAPGPLPPPPTPSSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

09933310101
TUSTOT 5523/660

FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTTATGGCTTACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGTTTCTCCTCCCATCAGTTATATTGGTATAAGCAACAGACTAATAACCAGGAACCCATC
AAAGTAGCAACCCCTAAGTACCTTACTTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
CCCTGCCCTCAATTTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCAGAACTCTGGGCAACAATACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGC
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCTGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAAGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

09973295.101501

CONFIDENTIAL

><subunit 1 of 1, 321 aa, 1 stop

MGILLGLLLLGHGLTVDITYGRPILEVPESVTGPWKGDVNLPCYTDPLQGYTQVLVKWLVRQS
DPVTIFLRDSSGDHIQQAKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRI SLQCQARGSPPI SYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSSEQHSDIVKFVVKDSSKLLKTKTEAPTMT
YPLKATSTVKQSWDWTDMGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR

amino acids 1-19

amino acids 149-152

amino acids 282-300

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTGCGA
GGCGCCCGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
GGGATGTCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAA
GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAATTTCTGCGAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGTGAC
AGAAGGAAGTGACCTGACTTTGAGTGAGTCACTCTGGCACAGAGCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCAAATCTAGGATT
GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAAGCTGTGTGGTGCGAGTAACGTACAGT
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCAGCCAGAGCAGAGCCTTCCAA
ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTTCTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTGAGATGAGCATTCTTCTTATACAATACCAAACAAGCAAA
AGGATGTAAGCTGATTCTGTGTAAGGATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT
ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACCTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTGATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCTCAAAT
CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT
TATCAACGTCTTAGAAAGAATTCTTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA
CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGEELTEGSDLTQLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

09978295-101501

FIGURE 25

GTGTTCCCTTTGCTCTCTCGCGCCAGTCTCTCTCTGTTCTCTCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
 GACGCGGGCTGAGTCCGCGCGGCTTCTCCCGCCTGGGCGGCTCGCCGCTGGGCGAGGTGCTGAGCGCCCCTAG
 AGCCTCCCTTGCCGCTCTCTCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCGGAGGCGGCGGTGATGCGGCGCTGGGCAGAAAGCAGCCGCGATTCCAGCTGCCCCGCGCGCCCGGGCG
 CCCCTGCGAGTCCCGGTTGAGCCATGGGGACCTCTCCGAGCAGCAGCACCCGCTCGCCTCTGCGAGCGCATC
 GCCCGCCGAGCCACAGCCACGATGATCGCGGCTCCCTTCTCTGCTTGGATTCTTAGCACCCACAGCTCAG
 CCAGAACAGAAAGGCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCGAGCTTGCCCT
 GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG
 ATTGAGAAATTACCTTGTGCTGCTTGAATGACCGAGAAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT
 ACCTGTGCCCCCATAAGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGACAGAGACTGAGGATGTGCGG
 TGTAAAGCAGTGTGCTCGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGT
 CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGACCAAGGAGACAGACAACCTCTGTGGCACACTCCCGTCCCTC
 TCCAGCTCCACCTCACCTTCCCTGGCACAGCCATCTTTCCAGCCCTGAGCACATGGAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAAGGCATGAATCAACAGAAATCAACTCTTCTGCTCTGTAGACCAAAGGTACTG
 AGTAGCATCCAGGAAGGGACAGTCCCTGACACACAAGCTCAGCAAGGGGGAGGAAGACGTAACAAGACCCCTC
 CCAAACCTTCAGGTAGTCAACACACAGCAAGGCCCCACCACAGACACATCTGAAGCTGCTGCGCTCCATGGAG
 GCCACTGGGGCGAGAACTCCAGCACGCCCATCAAGGCCCAAGAGGGGACATCTAGACAGAACTACACAAAG
 CATTTTGACATCAATGAGCATTGCGCTGGATGATTGTGCTTTCTGCTGCTGGTGTGTTGTGTTGTTGTTG
 TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGAAAAGGCA
 GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
 ATCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
 AGGAGGTTGCTGCTTCTCAATGGGTACACAGCCGACACGAGCGGGCTACGAGCTCTGCGAGCTGGGACC
 ATCCGGGGCCCCGAGGCCAGCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG
 AAGATTGCTGGGCTGATGGAAGACACCACCCAGCTGGAACTGACAACTAGCTCTCCGATGAGCCCCAGCCCG
 CTAGCCCGAGCCCCATCCCCAGCCCCAACCGGAACTTGAGAATTCGCTCTCTGACGGTGGAGCCTTCCCA
 CAGGACAAGAACAAGGCTTCTTCTGGATGAGTCCGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
 TCCGCGCTGAGCAGGAACGGTTCTTTATTAACAAAGAAAGAGGACACAGTGTGCGGCAGGTACGCTGGAC
 CCCGTGACTTGAGCCTATCTTTGATGACATGCTCCACTTCTAAATCCTGAGGAGCTGCGGTTGATTGAAGAG
 ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGGAATATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
 CTCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAATTACTCA
 ATTAGTGGCAGGGTGGTTTTTAATTTCTTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTTGT
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGCTTGAGTTCTTTCTCTCTC
 TCTCTCTTTTTTTTTTAAATAACTCTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAATGTTGTGAA
 ATACCCACCATAAAGTTTTTAAGTTCCATATTTCTCCATTTTGCCCTTCTATGTATTTTCAAGATTATTCG
 TGCACTTTAAATTTACTTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGCTCTTAACATTACACCTACTTTTT
 AAAACCAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTCTTAAAGATTAAAGAAATTTAAGA
 CCCATTGAGTTACTGTAATGCAATTCACCTTTGAGTTATCTTTAAATATGTCTGTATAGTTTCATATTCAATG
 CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC
 TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAATCTCAAGCCATCAGGATTTGCTATTAAAGTGGCTT
 GACAACTGGGCCACCAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCATTT
 GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
 TTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTGGTCTGTGGGATTCTTCAACCAAT
 ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTGCAACTATGCTCCATTACAAATG
 TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGTTTGTGG
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAACATTAGGTGTTTGTGA
 AAAAAAAA

09073205-101501

FOR THE

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCTGAAATAGTCAC
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTATTCCGATCGCTTTTTGGCC
TTGATGATTTGAAAATAAGTCTGTGTCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAAATGCCGTGCTCCAGGTGTTACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC
TGGGTTTTCCCAAGCTATGTGAGTTTCAAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATGTGAGGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAAGTGCACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCAGCCTCGTGGGTGGAACATGTCTTGCTCTCGCAG
TGGCCCTGGCAGGCGAGCCTTCAAGTTCCAGGGCTACCACTGTGCGGGGGCTCTGTCTATCAC
GCCCCGTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCAATGGA
CCATCCAGGTGGGTCTAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCTGCCCCAATCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCTGTCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGCTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTCACCTCCTTCCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCTGAGGTGATGAAGACAGCCCGATCCTCCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCCGGCACCA
GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTGTATTTTAGTAGAGAC
AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC
TGATCTTCACTAAGAACAAGAGAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC
ACTGCACGTTTTTCTCTAGGGACCAGAAACCAACCCACCCCTTTCTACTTCCAAGACTTAT
TTTACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT
TGTAGCATTTGGTGCTTGACGTATTATGTCTTTGATTCCAAATAATATGTTTCTTCCCT
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

09978295-101501

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLRVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVLTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCYVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHISKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDSSGGLVLCQERRLWKLVGATSFSGIGCAEVNKPQVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

105701-5628650

FIGURE 29

CCCACGGCTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTATTGCAACGGTCAAGGCTGGCTTGT
 GCCAGAACGGCGCGCGCGCGCGCACGACGACACACGCGGGGAACTTTTTTAAAAATGAAAGGCTAGAAGA
 GCTCAGCGCGCGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCCGGA
 CGCCCGGCCCCGGCTCGGCGCCCGCTGGGATGGTGACGCTCGCCGCGGGGCCGAGAGCTGCTGCACTGAAG
 GCGGCGACGATGGCAGCGCGCCCGCTGCCCGTGTCCCCCGCCCGCCCTCTGCTCGCCCTGGCCGGTGCTCT
 GCTCGCGCCCTGCGAGGCCCCGAGGGGTGAGCTTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCACTGCCCTCTGT
 TCGGAGTGGGACCTCTGGATCCCACTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTGCACT
 ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTACCGGAAAC
 CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACAGGGTCACTGTACTACCATGGACATGT
 ACGGGGATATTCTGATTACAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAATGA
 AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTCCAGCGAAGAAGCTGAAAAGCGT
 CCGGGGATCATGTGGATCACATCACACACCAAACTCGCTGCAAGAATGTGTTCCACCACCCTCTCAGAC
 ATGGGCAAGAAGGCATAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG
 AGAGTTTACAGGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAATAGAGATGCTAATCACGTTGACAA
 GTTTTACAGACCACTGAACATTGCGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCCATTACACGCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAATCCCA
 TGACAAATGCGCAGCTTGTCTAGTGGGTTTATTCCAAAGGACCAACCATCGGCATGGCCCAATCATGAGCATGTG
 CACGGCAGACCACTCTGGGGGAATTGTCTAGGACCACTCAGACAATCCCTTGGTGCAGCCGTGACCTGGCACA
 TGAGCTGGGCCACAATTTGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
 GGAGAGCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTAACTGCGGGAAGTCAGGGAGTCTTTCCGGGGCCA
 GAAGTGTGGGAACAGATTGTGGAAGAAGGAGAGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
 CTGCAATGCCACCACCTGTACCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
 GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC
 TCACTGCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
 CTGCCAGACTCAGGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
 GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAGTCTCGAAGAGTTCTTTGCCAAATGCGAGAT
 GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
 CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGACCCACGTGTACTTGGGCGATGA
 CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
 AAATATTAGTGTCTTTGGGGTTACAGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
 CTGCCACTGCGAGGCCCCTGGGCACCTCCCTTCTGTGACAAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
 CATCCGCAAGCAGAAGCAAGGCAGGAAGTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
 ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCCTGACCCAGTG
 CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
 TCCATGACAAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
 CAGTGCAAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAAAATGACATGCTTCAGTGCTGCTCCTGAG
 AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
 ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGTTTGGGCCAGTGTCCCTTTCCCAAGTGACACTCAGCCT
 TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTACGATTTATTATATGAAAT
 AGCAGGTTTTAGTTTTTAAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCAAGCAAACTGAATGGCAA
 TGAACCAAACTGGAGAAGAAGTAGGAGAAAGGGCGGTGAACCTTGGCTCTTTGCTGTGGACATGCGTGACCAGC
 AGTACTCAGGTTTGGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTACCAACCCCTTCATTTAACAGTAAGAA
 TGTAAAAAGTGAAAAACAATGTAAGAGCCTAACTCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
 GAAT

1097325.1054

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDISK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCCYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTFNL
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQROGKDLEKVKQRLIEIANHVDFK
YRPLNIRIVLVGVEVWDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGVCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVSXSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLOQGGRIILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRCQONISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGQGEFVGSGEHAASLTLL

Signal peptide:

amino acids 1-28

097325-10501

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

097EE95.10504
F0501.5622/660

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT
GAAACCATACTTTTACATTTTAAATGACAGGAAATGCTCACAATAATTGTTAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAACAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTTCGAAATCTGCCT
TTTTATAGATTTGTAAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGGTAAGGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTGT
CCTTTAACAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAACAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAAGTGGCT
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

09978295.101501

FIGURE 34

GCGCGGCGGAGAGCGCGGCCAGCCCCGCGCGATGCCCCGCGGCCAGGACGCGCTCCTCCCGCTGCTGGCCCCGCG
 CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCCGGGCCAGG
 AGGCGGCGGCGGCGGCGGCGGAGCGGGCCCCCGCGGCGAGCGGCGAGGACGGACAGGACCCGACAGCAAGCACC
 TGTACACGGCCGACATGTTACGCGACGGGATCCAGAGCGCGCGCACTTCGTTCATGTTCTTCGCGCCCTGGTGTG
 GACACTGCCAGCGGCTGCAGCCGACTTGGAAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
 ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCGAGGATACCCACCTTAA
 AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCAGACACTGGAAAACTGGATGC
 TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCGGGAAGTGAACCGCCAGTGCCCCGAGCTCAAGCAAG
 GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTGCAAGGCGACCACTTTATCAAGTTCTTCGCTC
 CGTGGTGTGGTCACTGCAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG
 TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCCGGAAACAGGTTCTGGGCTATCCCACTC
 TTCTCTGTTCCGAGATGGGAAAAAGGTGGATCAGTACCAAGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG
 TGGAGTCCGAGCTGCAGCGCACAGAGACTGAGCGAGCGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG
 CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA
 TAACCTTCATCAAGTTTTATGCTCCATGTTGTGGTCATTGTAAAGTCTGGCTCCTACTTGGGAGGAACTCTCTA
 AAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACCTGCTGAACGGGAATATCTGCAGCA
 AGTATTCGGTACGAGGTACCCACGTTATGCTTTTCCGAGGAGGGAAGAAAGTCACTGAGCACAGTGGAGGCA
 GAGACTTGACTCGTTACACCGCTTTGGCTGAGCCAGCGAAAGACGAACTTAGGAACACAGTTGGAGGTAC
 CTCTCCTGCCAGCTCCCGCACCTGCGTTTGGAGTTTCACTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
 GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTCCAAGCCACACACTCTACAG
 ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTCAGTGGCGATA
 TATCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA
 TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC
 CCACGAGTTCTGGAAAGGTGGCCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCAAGTTGACTCAATAC
 TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCGCGTGC
 TGGAGCTTCGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
 GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGCATACCTTGTCAAATCAGTTACTGTTTCAGGGGAT
 CCTTCTGTTTCTCACGGGGTGAAACATGCTTTAGTTCCCTCATGTTAACAGGAAGCCAGAGCCACATGAAGTGT
 TGGATGCTTCTCTAGAAAGGGTAGGCATGGAAAATTCACGAGGCTCATTCTCAGTATCTCATTAACCTCATGGA
 AAGATTCCAGTTGTTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCTGGGTATCCAGGGAGGC
 TCTGCAGCCCTGCTGAAGGGCCCTAAGTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
 CTTGCTATACTTGGTCTGCTTCAAGGAGGTGCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC
 CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
 ACTCATGCTGCTTGTGATTAAACACCTCTATCTCCCTGGGAATAAGCACATAAGGCTTAAGCTTAAGATA
 GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGCATCCAACACTCTTACCCACCT
 CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
 CTGCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG
 TATGGTTCAAGATAATTCTTTTTTAAAAAAACCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
 CACAACCTCAGCTTTGCATCAGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTGTTGTTTACACTAT
 GATACTTCTAAATAAACTCTTTTTTTTTAA

10501 "56234650

SECRET

><subunit 1 of 1, 432 aa, 1 stop

MPARPGRLPLLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNMEDAKVYVAKVDCTAH
SDVCSAQGVRYPTLKLFPKGQBAVKYQGPRDFQTLNWMQLTLNEEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIFKFFAPWCGHCKALAPTWEQIALGLEHSETVKIGKVDCT
QHLYELCSGNQVRGYPTLLWFRDGGKVDQYKGRDLESLEYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

amino acids 1-32

FIGURE 36

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTA
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTTATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAA

10978295-101501

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRTAÆVCATHHTISPGPKGDDGEKGDPGEEG
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY
RKFBVGQLDISIARLKTSMKFVKNVIAIGIRETEEFYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

109701-5623/660

FIGURE 38

GGTTCATCGATTCTGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTTCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCCTTTCGGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACCTGGCCAGCAGCGCGCGCGC
ACACCTTTCTCATTACAGGCTCGCGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGCGCAGCAG
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTTCTGTGGCTCTG
GTTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC
CCCTGCTGCACTGCCTCCGCGAGCTGCGGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG
GAGTCCCTGGAGCCGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC
ACCTCTGGCACCACGGGCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAG
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCGGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGGCTTTACAAGC
ATATCTTCCCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTTCGGGACCC
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
GCAGTCCCCATTCCTGGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGG
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCCAGATTCTTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCCTACCTGCCCCCTACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGG
CCGTTGCAGGTGTACTGGGCTGTGAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCCAACTTGTATTATGCAG

0973295 "101501

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAAIGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL
LLLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRRTAFVPTAL
RRGPILLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGFPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGORGAVGRASW
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GK
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

00070205-101501
10070205-101501

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
 CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATAACACTCGCTCTC
 GCTTGTCCATCTCCCTCCCGGGGAGCCGGCGCGCTCCCACCTTTGCCGCACACTCCGGC
 GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC
 CCATGGTGGTTTTTTAAACACTTCTTTTCTTCTCTTCTCGTTTTGATTGCACCGTTTTCCA
 TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT
 CCATCTGGCTTATAAAAGTTTGTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCCTCGG
 CTGGCAGAAGGGGGTGACGCTGGGCAGCGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT
 CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTGTATG
 TTGCACCATGCTTCTTGATCGGGGCTGTGATTCTTCCCCCTTGGGGCTGCTGCTCTCCC
 TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC
 AAGGGATTGAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
 TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAGCAAAC
 TCGAATTTGAAAACCTTGTTGAAGAGACAAGCCATTTTGTGCGCACCACCTTTGTGTCCAGG
 CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA
 TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTGAGAAGTCTTCCAGGACCTCT
 TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC
 TTTTGGGCTCGGCTCCTGGAACGGATGTTTCACTGATAAAACCCTCAGTATCACTTCAGTGA
 AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC
 GGAAACTGAAGATTGAGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
 ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTGAGCCCAACCCAGGGTGTATCCG
 TGCCCTCATGAAGATGCTGTACTGCCCATAGTGTGCGGGGCTTCCCACTGTGAGGCCCTGCA
 ACACTACTGTCTCAACGTGATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
 TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
 TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
 ACAGCATGCAGGTGTCTGCAAAGGTCTTTGAGGGATGTGGTCAGCCCAACCTGCTCCAGCC
 CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA
 CTAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
 AATTGAAGCTCTCTAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC
 GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
 GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA
 TCACTCGGCCTGACACTTTTATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
 CTAAAAAACGCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
 CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTTTGTACCA
 CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC
 CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGCAGAGACTGTGCAGATA
 ATCTTGGGTTTTTGGTGCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT
 TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG
 CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG
 CTTCCTCTTTCTTTCAGCTATCTGTGGGGACCTTGTATTATTCTAGAGAGAATTCTTACTCAA
 ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTGCTTTTATGCTGCAGAAGTAAAGGAAT
 CTCACGTTGTGAGGGTTTTTTTTTCTCATTAAAT

00070205-101501

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTTELKRYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFS E DY
LECVSKYTDQLKPFQDVPRK LKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNL FIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNQENSMQVS AKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

09973295.101501

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTGACGCGCCTGCGCCGGGTGCGCCAACTACGCAAGACCAAGCGGGCTCCGCGCGGACCGGGCCGGGGC
TAGGGACCCGGCTTTGGCCCTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCGCGCTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGGAATAAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGAGTTCTTTCCAGGTGTGCGGACCGCAGGACAGACGGCCGA
TCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAAGCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA
AAAGTTCTGTCCACTGTGATTCTCAATTCTTGCTTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA
ACTTTTTCTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGAGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGAGTCCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGATTCTTGCCAGGTGGAGAGTCTTCAACGCTCTGTGGGTGCATG
TGTGCGCCCGCAGCGGCGCGGGCGCGTGGTTCTCCGCTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGGCTGTGCGGGGCATCCGCTCCGCTTCTCCACAGGCCTGTGTCTGTCTGAAAGATGCTAGCAATGGGG
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGG
AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCAGCCCCATCTCA
TTTTCATCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCAAGGATCTGAGATTAAACACCTACTCTTG
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACTGTTTAC
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCCGAAAAATGGCACT
TGGGTTTTAACAGAAAAGATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG
GGGATTACTATACACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAAAAGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA
ACCCACAAAAGCCTATATTTTTATATACTGCCATCAAGCTGTTTCACTTCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGTATGCTGCCATGCTTTCTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAAGTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG
ACTGGTACCCCACTCTCATTTCAGTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCGAGTAGATATTTTGATAACATTGACCCCTATACACCAAGGC
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCTACGGAGGCTCTCACAGTTCAACAAAAC
TGCAGTGCCGGTCAGGTATCCCCCAAGACCCCAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAAACCAAGAAAAAGGCCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCGCCCACTGAAAACTGTCTGCTCAGTG
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAAAGTG
GTGAGTCTGAGTTCCACTGCTGTGCTTCACTCAACTGACCAAACTGCTTTGAATTATAGGAGGAGAAACAATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

0073295.101501

FIGURE 42B

AGTCAAAGATTGTGTACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTCAATGA
CACTTGGGTTTMTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC
ACAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTTCAGTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTGTTTTATAAAAAGTTATGCAAATGACTTTTATTTTTATTTCTGCATACCATTAGAAGA
ATTTTATTTCAATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAAACATCATTTCAGAAAACTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCAATGTTTGTGCAGAGTTGAGACAACCTTTATGTTTTCTATCATAACTATTTATGTATCTT
AATTATTAAAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAATCTCTAGCTAAAATT
GTATCATTTGGTCTCAAATAAAAAATCTTTACTAATAGGCAATGAAGGAATGGTTTGCTAACAACCCACAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCATAATAAATACTAA
TATTTATATTAGGTTGGTGCAAAACCTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAAACCCC
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCAATCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCTGGTGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTAC
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATGGGTAAGATGATTTAAATGATTTTAAATTTTAAATTTTATTTCTAGAATATAT
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

105101-56232660

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNSSIIYYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVFVHSPLLKNKGTVCCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

0978296.101501

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCTCTGCCCCGGAGCCTTGCCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAACCT
GGGGTCTGTCACTATGGAACATAAAGTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGGGTGGGACCAACAAAT
GCAGATGCTTTCCAGGATACACCGGGAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA
ACTGTCAAGTACAGCTGTGAAGACACAGAAGAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGTCA
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAATTAATAATGTTACCCAGAACCCACCAGGACTCC
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAT
CTCATGGAGGTAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCGGCCTTGGCAGGTACAAGAAAGACATTGGCCGATTGAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAACTTCGAGTGTGTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAATTCAGTTGTATCAAGGAAGTGAATGC
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTCAAGTCCCTGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAACTTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCTTTCTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACTTTCTA
GAAAATAGAAAAAAAGCACAGAGAAATGTTTAACTGTTTGAAGTCTTATGATACTTCTTGA
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

56234650

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECEVGPKNKRCFPGYTGKTCSDVNECGMKPRPCQHRCVNTHGSKYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

09978295-101501

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGGAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTG CAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTC CATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGGAATGTCCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTCT
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACCAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTAAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

09973255-101501

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQSRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

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T05T01 56282660

FIGURE 48

CGACGTGGGCACCGCCATCAGCTGTTGCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTTGGTCTTCAAGCCGCTCAGCGTGCTGTG
GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCTCACTGCTGCCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCTGGT
CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCGCCCATCGCTTCC
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACCTGTATCTACAACCAGCT
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCCAGCCTG
GGGTGCAGGGCCCCCTGTGAGGGAGATTCCGGGGGGCCTGTGCTGTGCTCGAGCCTGACGGA
CACTGGGTTTCAAGCTGGCATCATCAGCTTTGTCATCAAGCTGTGCCAGGAGGACGCTCCTGT
GCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAAGGGGGCAGCTT
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCCTGGGGCCTAG
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
TGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG
CATGAGGTGAGGGGCACATGGTTCTCGCCGGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCAATGGCATTACTGCCCTGTCTCCCCACCCCTGTCATGTGTGATTCCAGGCAC
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC
AGGCGTCTCAGCTTTCTCTCTCTTTACTCTTTTCAATACAATCAGCCAGCCACGTTGTTT
TGAAAATTTCTTTTFTTGGGGGGCAGCAGTTTCTCTTTTAACTTAAATAAATTGTTAC
AAAATAAAA

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FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPTTHTPLCLPQPAHRFFPGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARGMLCGGPQPGVQGPCQGDSSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLGPRACSRHLHAAPGGDGSPIPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPE
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

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FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG
CCCAGCTGTTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTTCAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCCAACAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTC
TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAAACGA
GCAGGGCTTGTTTGATGTGCACAGCGTCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCAGCAACCCCGTGTGTCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGG
CAGCCTATGACATTCACCCCGAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCTGTGTCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCTACCCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTACCCCGGCCCTTGTTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGGCCCTCAACATCTCCTGGAGCTAGAAGCTGTTTCCTTTTC
CCCTCCTTCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCACCACCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGC
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

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FIGURE 52

TTCTGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGTCTGAAGCCCTTGTCCGTAAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCCTTGCTTCAGCAACATGAGGCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTCTGTCACCTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCTCTGCCATCGCAAGACCAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAAAGCTCATCATTCCTCCTGC
TCTGGGCTATGGAAGAAGGAAAAGGTAATAATCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGGAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCAGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTATATATTTT
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACAGGTTATAGCACAAATTAGCACCTATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAGCCCTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAACCTGGCTCTGAGTCTCTGCTTGAGGACCAGGAAAA
TGGTTGTTGGACCTGACTTGTAAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACCTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAAATAGGACAAATCATTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCGTGAATCCCAGCACCTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

0073245-101501

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS
L
FHSTHKHNNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDKDGFIAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

00078295-101501

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FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEBEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

105101" 55222650

FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGGTGGAGTTCTCAGG
GAACCCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCCC

09078295.101501

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAAC TGCTACATCATGAACCCCCC

09072295.1015014

FIGURE 58

TCGGGCGACCGTGTACACCATGGGCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT
 TCCTCTTGCTGTCTAATGCTGCTCGCGAACCCAGCGCTCCCGGCCGACGTCACCCCCAGTGGTGTGGTCC
 CTGGTGATTTGGGTAAACCACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCCTACCTCTGCTCCAAGAAGA
 CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAAGTGTGCTGCCCTGTCTATCATTGACTGCTGGATTGACAATA
 TCAGGCTGGTTTACAACAAACATCCAGGGCCACCCAGTTTCTGTATGGTGTGGATGTACGTGTCCCTGGCTTG
 GGAAGACCTTCTCACTGGAGTTCTGGACCCAGCAAAAGCAGCGTGGGTTCTTATTTCCACACCATGGTGGAGA
 GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG
 AAAACGGGGCCCTACTTCTGGCCCTCCGCGAGATGTACGAGGAGTGTACAGCTGTATGGGGGCCCGTGGTGC
 TGGTTGCCCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCTGGAAGGACAAGT
 ATATCCGGGGCCTTCGTGTCACTGGGTGGCCCTGGGGGGGCGTGGCCAAGACCTGCGCGTCTCTGGCTTCAGGAG
 ACAACAACCGGATCCAGTCACTGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTGAGTGTCTCCACCAGCTGGC
 TGTGCCCCACACTACACATGCTGACCTGAGAAGGTGTTCTGTGCAGACACCCACAATCAACTACACACTGCGGG
 ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
 AAGCCACGATGCCACCTGGCGTGCAGCTGCCTGCTATGGTACTGGCGTCCCCACACAGACTCCTTCTACT
 ATGAGAGCTTCCCTGACCGTGAACCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTGAAGAGTGCCC
 TGCAGTGCCAGGCTGGCAGAGCCGCCAGGAGCACCAGTGTGCTGTCAGGAGCTGCCAGGCAGCGAGCAGATCG
 AGATGCTGGCCAACGCCACCACCTGGCCTATCTGAAACGTGTGCTCCTTGGGGCCCTGACTCCTGTGCCACAGGA
 CTCTGTGGCTCGGCCCTGGACCTGTGTTGGCCTCTGGGGCTGTCTATGGCCACCGCTTTTGCAAAGTTTGTA
 CTCACCATTCAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTCTGTTGTTATCCTTTCTCT
 GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGA
 ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCAGTCCCTGCTGGGGCCATG
 TGTCCCCCTATTCTGTGGGCTTTTCTACTTGGCTACTGGGCCCTGGCCCCCGCAGCCTTCTATGAGGGATGTT
 ACTGGGCTGTGGTCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCCCTTCCACACACCA
 GCCACAGATAGGCCTGCCACTGGTCAAGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
 TGAAGTGGCTTCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTGCGTCTTCTGTTGGTTCCAGGC
 CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG
 CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGATGTGCTATTGGCCCCAGGACTGAAGCTGC
 CTCCCTTCAACCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGA
 GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCATCA
 CACTGCCACCTGCCCCAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC
 CCTGGCCAGCAGCCAGCTTAGTGCTGGGACTAGCCAGAACTTGAATGGGACCCCTGAGAGAGCCAGGGGTCCCC
 TGAGGGCCCCCTAGGGGCTTTCTGTCTGCCCGAGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT
 CAGGGCTGCCCTTATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT
 GGGGTTCCCAAAGACGCTTCAAGGCTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG
 TTGCATACATGCTGGCATCTGTCTCCCTTGTCTCTGAGTGGCCCCCATGGGGCTCTGAGCAGGCTGTATCTG
 GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

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 00800

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
FVIGPLKIREQQRSVSTSWLLPYNITWSPEKVVFQTPPTINYTLRDYRKFFQDIGFEDGWL
MQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FOR 5623466

FIGURE 60

CGGACGCGTGCGCGGACGCGTGCGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAGTGCCA
GCCCCCTCTTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCCGGTCCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCTCA
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

00504 5628460

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDILLFSALWTFWLVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

05978295-101504

FIGURE 62

GAGCCACCTACCTGCTCCGAGGCCAGGCCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCCGTGGCCGAGGCCCGCCAGGTGGCTGGCGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG
 ATGTTCAAGGCCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGCTACCTCCGCTGGTGCCCTGTTTGTGCTGCTG
 GCGCTGCTCGTGTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGC
 CAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGTGCC
 TTCGCGAGTGAAACCGCCAAAGCCAGAGATGCTCAAGGAGCTCATCACCAGCACCCGCTGGGAACCTTACTAC
 AACTCCAGCTCCGCTCTATTCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTCATTCTCCAAATCCCCGAG
 CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGAGGCACTGCTGGTGAGGAGCTGCTGTCCACAGTCAACAGC
 TCGGCTGCCGTCCTCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA
 GACATAGCTGCATGGAATTCACGCTGGGTGTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG
 AAGGGCCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACTCCGG
 CTGGAGTGGACGCTGGCAGAGTGGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTC
 ATCACCCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGAGGTTCTGGCGTCCGGGGCCATCATCGCGCTC
 GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGCTGGTCTTCCAGCCCTGT
 GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCAGGGCGTCTCAGCACCCCGTACTTCCCCAGCTACTAC
 TCAGCCCAAAACCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC
 TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT
 GGCTTGGCATCTCTGCAGCCCTACGCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC
 TCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCACTCGGACCCCTGCCCTGGA
 GAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCTGTGATGGGGTCAAGGACTGCCCAACGGCCTGGAT
 GAGAGAAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACAGCACATGCATCTACTGCCCAAGGTCTGT
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACAC
 TTCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCGCAGTGTGATGGGCGGCCGACTGCAGGGACGGC
 TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGCACTTGTGGTGGAGCTGTGTCTCCGAG
 GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC
 TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGCTGTGGACCGTGTCTCTGGGC
 AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGCTCTTCAAGGTGAGCCGCTGCTCTGCAACCCGTACAC
 GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGGCTCGGCCCGCGTGC
 CCGCTCTGCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGCCTGCAGTGTGATACGGGCTGGGGCGCCTTG
 CGCAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCACTTGATCCACAGGACCTGTGCAGCGAG
 GCCTATCGCTACCAAGGTGACGCCACGCTGCTGTGTGCCGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGT
 GACTCAGGTGTCCGCTGGTGTGCAAGGCACCTCAGTGGCCGCTGGTTCTTGGCGGGCTGGTCACTGGGGCCTG
 GGCTGTGGCCGGCCTAACTACTTCCGGCTTACACCCGCATCAGGTGTGATCAGCTGGATCCAGCAAGTGGTG
 ACCTGAAGGAATGCCCCCTGCAAGCAGGGCCCACTCCTGGACTCAGAGAGCCAGGGCAACTGCCAAGCAGG
 GGGACAAGTATTCTGGCGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC
 CTGATGTCTGCTCCAGTGTGCGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCTGAGGACC
 CAGGCCACACCCAGCCCTTCTGCCTCCCAATTCTCTCTCTCCGTCCCTTCTTCCACTGCTGCCTAATGCAAG
 GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG
 CTGTTTGGGCAGCCTTGCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCCTGGTCTAACTTGGGATCTGGGAAT
 GGAAGGTGCTCCCATCGGAGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGCCCTGCTGCCACTGTAAGCCAA
 AAGGTGGGGAAGTCTGACTCCAGGGTCTTGGCCCCACCCCTGCCTGCCACCTGGGCGCTCAGCCCCAGACCT
 CACTGGGAGGTGAGCTCAGCTGCCCTTGGAAATAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAA

0907295.10501

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YINSSSVYSFGEGPLTCFFWFILQIPEHRLMLSPPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCRYRYSYVQGQVLRKGPDLASSCLWHLQGPDLML
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLPSTPYFPSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTQGGWTIQNRRLCGLRILOPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNLGCVLPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDCQPDCLNGSDEEQCEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAACHCFQEDSMASVT
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

09070205 101501

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTGCACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGTCTGTGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC
CGTCTGCCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGAATCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

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FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTTAAA
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCCGCCACAG
CCAGCCCCTTAGAAGACTGCAGTTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGGATGTCTCCACACCTACACGCGTTCTTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCTTCCAGTGCACT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACAATCCTAGCCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRSTKDP EHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

09578293.101501

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCGGGCCGAGCCACCTCTTCCCCTCCCCCGC
TTCCCTGTGCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACAGGCCAGACCAGGGGCGCTCG
CTGCTTGGGGCGGGCTGTAGGCGAGGGCGCGCCCACTGCGGAGACCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGGCGCGCGGACGGAGAAAACAACTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
CCGCTCCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGGCGCCCGGGCTCCGCCGCGACCCCATCGGGTAGACCAAGAAGCTCCGGGACCCCTCCG
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGTCTTTAGAAGTGAGGGCACCTTTACAGA
GGCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCTGGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACCTACAGCTATG
CTGGGGCCAGAGCACCCCATGGGCCAGGGCTTCCCTGCTCTCTACAGCCAAGATTGGCTGATGTGCTGCAGGAAG
AGTTTCAGTGCTGAACCAACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCTCCTGCTGCTGCAATG
TCACCTTGGAGACTTCTATGGGCTCTTCTCCTCTCTGGATATACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGTGAGCCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCTTGAGAGCTCCGACTACTGCGTAGTCTCACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTGTGTCTTACCACACAGTTGCTTGGAGC
ATGGTGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCTTGGGACAGACCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCTTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGTGTCACCT
CTGTGTCACAGCCTGCTACCTGCTGTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGCGCATTGGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATACAG
CTGCAGTCAATGGCAGCCTAGTGTGCGGCTGCTCCTGGTTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGAGCAGCAGGCACCCC
CTTCTACGGGCAGCTCATTTGCCAGGGTGCCATCCACCTGTAGAAGACTTTCTTACAGAGAATCCTTAATGATA
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCGCGCTGCTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGCTCTCCGCCGCTGGGGCTTGCTCCCTCGAA
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCCCTTGAGGCCCTAGATG
GTGGCACAGGTCCAGCCCGTGGGGCGGGGCTGAGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCCATCA
AGGCTCCCCCTCCATCTGCTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGAGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGAGCCCCCTGGACCCACACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCCTCC
ACCACTTCCCTCCCTGTCCCTGGATTTCAGGCACTTGGTGGGCTCCCGTTGACCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACTGCTCCCCACGCCACCACTTTGGGTGGCTGTTTTTAAAAAGTAAAGTCTTCTAGAGGATCATA
GGTCTGGACACTCCATCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA
CCCTCCAGCCCCCAAGGGGAGGATTGGGCGAAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG
CTCAGAAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGCCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

105101 56234660

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHFPDRIIFPNHACEDPPAVLLEVQGTLQRP LVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSR LTLRSPLQLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRC DGV DACGDGSD EAGCSDPFPGLTPRP
VPSLPCNVTLEDFYGVFSSPGYTHLASVSH PQSCHWLLDPHDGRRLAVRFTALDLGF GDAVH
VYDGP GPPESSRLRLSLTHFSNGKAVTVETLSGQAVVS YHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFR CRDEKCVYETWVCDGQPD CADGSDEWDCS
YVLPRKVITA AAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIP PVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGR LMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTG PAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRL LPSLGPPGPTRSPPGPHTAV
LLEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FOR 523250

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAGAAGTTTGTAAATTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAA

00078295.101504

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

105701 55232650

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACCTGTGACAGCAGTATGCTGTNTTGCCGAC

09578295.101501

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCCGCCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCCGCCAACTTCTTGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC
CCATGATGGGGGCCGGCTGAATTATGAATGTTACCGATTCCGGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGCTTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLR
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSRRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIIVLLLLPFRC
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

09078295.101501
105101.56232550

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCGTCGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCACTGTGCGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCACTGAGGACTC
AGAGGCCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTCTGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCTCGGAATAAAGCGCGTTGACCGCCAAA
AAAAAAAAAAAAAAAAA

097323.10501

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amino acids 37-49 and 114-124

FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCTGCCCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG
 GACTCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCAGGGCCCTGGCCCTGCCAGGATGAGCTGC
 CAAGCCTCAGGCCAGCCACCTCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCCTGAGCATGGTGCCCCCAGAC
 CCACACCACCTCCTGCTGATGGGACCTTCTGCTGCTACAGCCCCCTGCCGGGGACATGCCACGATGGCCAG
 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAAGAGGGCGCT
 CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG
 TTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG
 GCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG
 ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGTTTCCATCCAGGAGCCC
 CAGGACTACACGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAAATGTGACACTGCTGAACCCGGAT
 CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTCACTGGCCCTGCTGCGCCTGCCCAA
 TCTTACACGGCCTTGTTCAGGACCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC
 GGCTGGCAGAGCCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC
 CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAAAAGTGCCAGTGCCCCACCTCAGGAA
 GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCAACACCTGCTGAAAAACCAATGGCATC
 ATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACAGCCAACTGGACTGTAGTTGGTGAGCAG
 ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTCAAGTGGCTGCACTCACTGGTGTGGAGCT
 GGGGAGCCCAAGTACCTGTCTGCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCAGTGAGCAT
 GGTCCCTGGACCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCTGAGGTCATTGCCACCTGCGGTGTGCACTC
 TGGCTGCTGCTTCTGGGCACCGCGTGTGTATCCACCGCGGCGGAGCTAGGGTGCACCTGGGGCCAGGCTCTG
 TACAGATATACAGTGAGGATGCCATCCTAAACACAGGATGGATCACAGTGAATCCAGTGGTTGGCAGACACT
 TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCTCAGCAGTCCGCTGGGGGCGGATGCCCGG
 GACCCACTAGACTGTCTGCTCCTTGTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCTGCTTCCAGACACC
 AGCACTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCAGGTCCCAGCT
 GTCAGGCGCCTCCACCCCACTGGCCAGCTCTCCAGCCCTGTTCCAGCTCAGACAGCCTCTGCGAGCCGAGG
 GGACTCTCTCTCCCGCTTGTCTCTGGCCCCCTGCAGAGGCTTGGAAAGGCCAAAAGAAGCAGGAGCTGCAGCAT
 GCCAACAGTTCCTCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCTGTGAGTTAGGAAATAGAGGTTCC
 AAGAACCCTTCCCAAAGCCAGGAGCTGTGCCCAAGCTCTGGTTGCTGGCGGCGCCTGGGACCGGAACTCCTC
 AGCTCCTCAAATGAGCTGGTTACTCGTCACTCCTCCAGCAGCCCTCTTCTCATGAAACTCCCCAACTCAG
 AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCTGCTGCCAGCAGCCCCCATCCCCATC
 CTTAGCCCTGCACTCCCCCTAGCCCCCAGGCTCTTCCCTCTCTGGCCCCAGCCAGCTTCCAGTCCGCTGTCC
 AGCTCCTCACTGTCTATCCCTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA
 CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT
 GGGTACATCAGCGTCCCAACAGCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG
 GGAGTCTTGTGTGCCACCTCGGCCCTGCTCACCCTCCAGCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC
 TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGCTCCTCCGATGGCTCCTTCTCGCTGAT
 GCTCACTTGTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCAGGGAGGCAGACTGC
 GTCTTCATAGATGCCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCTG
 TGGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGGCTGGGAAGGGGGATGCCTCCC
 TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCAGCTCCACTGTCTGATGCCCAAGGCTGGTGCTTCTCCT
 GTAGATTACTCTGAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCCAAG
 ACCTGGGCTGTGGTGTGTGGGTCTTGGCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG
 TTCTCCTCCACGATTGTGAAAAACAAATGAAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA
 ACATCATCTCCACCTGACTCCTAGCCACTGCTTCTCCTCTGTGCCATCCACTCCCAACCACAGGTGTGTTTGGC
 CTGAGGAGCAGCCCTGCTGCTCTTCCCCACCATTTGGATCAAGGAAGTGGAGGAGCCAGAGGTGCCTTT
 GTGGAGGACAGCAGTGGCTGCTGGGAGAGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCT
 GGGCCCCCTCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAGAAAAATAATTATGAATGCCACTG
 AGGCACTGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG
 TATGAGACCGTAGGTCAAAGACCATCTCGTACTGTGTACTATGAGCTTAAGAAATTTGATACCATAAAAT
 GGTAAAAA

00973295.101501

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGPGRPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLLP
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQGRHTVSGGSLLMARAEKSDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGFW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSTPARPSPQVPAVRRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPDPDSQISSQRSQLHCRMPKAGASPDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

105336-55234660

FIGURE 78

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTTGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGTTTCCAGGACCCTGCTGTCTCCTCCCTCCCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCCTGGTGTGCTGAGCCTTCTGTGAGC
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC
 CTTTCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGTCATGTTCCA
 GCCTGACCTAGAACGCTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGC
 CTCATGCCCAGTGTGCGACCCTGCCTTCTCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCCAGTGACTGTGCACTTGAGTTTGAGGGCCAGTGGGCTG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTGGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGTCTAAG
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTTTCTTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT
 CTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTTCACTCTCCCAAATGCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTGTTCAAGTATGCAAACTTGGAAG
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTACCCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTGTACTTCTTCCACTCTTTCTTCTTACATAATTTGCCGGTGTCTT
 TTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

105101" 55224560

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYABEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQTETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

00073295.101501

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCAACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCCGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCTTGACCTAGGCTTGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

09072295-101501

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTNPVENVCRMYSDDLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

0057503510504

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCCTGCGTTC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCGTGGTGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCCCGCGGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGGAACCGGCGCTGGAAGTCTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGAAGTCCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACAGAGTGGGGAGCT
GGAGAAGTGGCGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCAGTGGTCAG
GATGCTCTGACAAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG
GAAGGCCATCCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGAGATTGCACACGTGCCGATGACCGCCTGCCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACACCTACCCCAAGA
GATACTGGTTGTATTTTTTGTTCGGTTTGGTTTGGGTCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTCATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAGAACTCTTAAGTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCACTCATGCCCGAGTCACCTTTTACAGCGCTGTTCTCCATGAAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCGAGTCACCTTTACAGCACTGTTCTC

097395.101504

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPGKVVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

0072295.10504

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGG
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCCTCGAAGCAGACGGCGGGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCCAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACCTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTTACGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCTATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACTGCTGACCCCCGCCAGTGCCCTGGAGCCGCGCCATTGCAGCATGTCTGTA
TCTTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCAGCAGACCCAAACCTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

09972295.10501

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLRLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVLTQGLAEAGRGREDVRTLEFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

POST "56352.DNA"

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCTTTCTCCCACGTCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTTGGCCGGCCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCCAGCCCGGCCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTCTGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCTGCTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCCGCAGCCCCCTGGGGCCCCCGG
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG
GGTTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG
TCCAGGGGCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAA

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGG
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGGTC
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACCTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCGCTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCTTCGAGGGCTCCTGCTACTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTCAAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCTATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACCTGCTGACCCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCTTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAAACCTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLRLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVLTQGLAEAGRGREDVRTLFRALAEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENCVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

1097225.10501

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCTTTCTCCCACGTCTTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTTGGCCGGCCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCCGGCCGCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCTGGCCACTCTCGGCGCCGCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTACGTAAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG
CGCTGCAGAGCGTGACGAGGTGTTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTCTGTGGGCGTGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCTCTCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCTGCTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCCCAACAACGGGAGCCCCCTGCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGACGCCCTGGGGCCCCCG
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCGAGGGCACAGGG
GGTTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG
TCCAGGGGCCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTGCGTTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

COLETTI

><subunit 1 of 1, 331 aa, 1 stop

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIBAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFGVDSLDCGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAAGTGTGTTGGTGTCCCTGTCTTGCGTGA
TATTGACAAACTGAAGCTTTCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAACATA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACCTTTGTTTTGGAAGCTTATTATGACAATACCATTTTTTTCATAGAGTTGTGCCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCAATTCACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT
TAACAATAAGCATAACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGATGAAAAGAACCCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCACTGAAGAGCTCAGAAAAGAAGCAAGACAATTTAAACGGGAACTCTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGGTGTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG
TACATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVN RVVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKS
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDTFEIIYDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

09973255-10504

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTTCGCCTTGCTGACGGCGTGC
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
GTGGCCGCGGGCGGGACCAGCACAGGCGGGCGTTCCTTCCTTCGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
CTCCTTCAAGTGGTTCCTTGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCTTGACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAA
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAG
TGCAGTGGCAGCATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG
ATGTACGTGACAGCAGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCGCGCGCGCGCGCGCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
CGGGAGGCGCCTTCATCGTGGGGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCCG
GAGAAAGTGGTGTGGTGTTCCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACACAGATGGCGGCTCTGCGCTGGGCT
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCTGTTTCGGCCAGTGGCG
GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCATCGGGC
CATTTCCCAGAGTGGCACCGCGTTATTTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
CCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCCAGATGACCCCTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCATTGGCTCTTGCCCTTATAATATCACCAGGAGCAGGT
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTTTCGTGTATGCCACACTGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC
TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACACTGTGCTCAGCTCTCAGCCTCAGGACAACCTCTTTTTCCTTCTTCAAATCCT
CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC
CCCTGTCACTGCACCCAGCTTGGCATTTACCATCCATCCTGCTCAACCTTGTTCTGTCTGT
TCACATTGGCCTGGAGGCCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPPFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

U997899.10594

FIGURE 92

GAGAACAGGCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
 GCTGTCTCTCGTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
 AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA
 CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
 CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC
 GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAGTGTCTCCTTGGTGATCAGAGACGCGCAG
 ATGCAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
 CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC
 ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
 GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTATCAGCATTTCACGTGACAACAC
 GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGT
 TCCTGCGGCTCCTCTGTGTGTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGTCAG
 AACAGAGTCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
 GGTGAAGGCTGGGGATTGAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC
 AGCGAGCCCTGGACCTCTCTGTGCAGTATCTCCAGAGAACCTGAGAGTGATGGTTTTCCAA
 GCAAACAGGACAGTCTCTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCA
 AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
 GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCCGGGTCTGGAGCTGCCTCGGGTT
 CAAGTGGAGCACGAAGGAGAGTTACATGACCGCTCGGCACCCACTGGGCTCCAGCAGCT
 CTCTCTCAGCCTCTCCGTGCACCTATAAGAAGGAGTCTCATCTCAACGGCATTCTCCAACGGAG
 CGTTTTCTGGGAATCGGCATCACGGCTCTTCTTTTTCTCTGCCTGGCCCTGATCATCATGAAG
 ATTTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC
 GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
 AAGCCACACCAAACAGTCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAG
 AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGC
 CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
 GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC
 CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
 GTTGAAGATAACAGAGTGCAAAGTTTCTTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCT
 CTCTCTTTCTCTCTCTTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC
 CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGGGAGTTCGAGACCAGCCTG
 GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG
 CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
 AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
 TCTCAAAAAAAAATCCTCCAAATGGGTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTA
 AGGTGGGTGGATTGCTTGAGCCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC
 ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT
 CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
 TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG
 TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA
 ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCTCACTGCTACACTCCT
 GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
 AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA
 GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT
 TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAAA

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVMSTRGRFQLTGDPKGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSTFPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQSPDGVLELPRVQVEHEGEFTCHARHP
LGSQHVLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins
signature.**

amino acids 365-371

0903295-101501

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCGATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACCTTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTTCGCAACATTGTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTAAA
AAAGAAAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCTTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAAACAATTCAAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTTAACTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA
TTTGGGTTTTATTTTTTTGACTTTGGGTTTTAAACAACGGAGAAAACAGATTCTATTTCTGGA
GAAAAGTGAAGATTTAGAGAGAATATATTCGAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTGAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCCTCTTTTGATTCCCTCCAGACCTACGCTTTTGGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTCTGTCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAATTTTTTAAAAGTGCTAATGTGTATTCGAACCCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAAGTACCTACATGCTGTCATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG
TAGGAAGATATTTAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT
TTAAA

09973295.101501

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS D
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAE MDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHFHYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

09073295 "101501
T0501" 56234660

FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTTCGCAAACATTTGACATTATT

09978295.101501

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGCGCGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTCCTCCGCGGGG
CCCAGCCACCTTCGGGAGTCCGGGTGCCCACCTGCAAACTCTCCGCCTTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCTTCTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTGGCATCCTCCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCATGACCCATGACCCAGT
CAATGCCAGGTACGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCC
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACTAGGAC
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA
ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCA
ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTCTATTAAAA
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAAT
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC
TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCCTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAATTTGGAGGCAAATCTTTCTGCATG
ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACACAACCTTTATTGATTGAATTTTTAAGCTACTTATTCATAGTTTTATATCCCCCTAACT
ACCTTTTTTGTTCCCCATTCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT
CACTGCCTTCTCTCTACCACTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCACTGCTTCTCTCTACCACTCTATTTCCACTGAACAAAACCTACGCACATAC
CTTCATGTGGCTCAGTGCCCTTCTCTCTACCACTCTATTTCCATTCTTTCACTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAATTCCTGATCTTCCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTAT
ACTAAGGGAAAGAATTGAGGAATTAAGTGCATACGTTTTGGTGTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

10501 "5225" 0501

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI~~L~~AF~~L~~GWIGAI~~V~~STALPQWRIYSYAGDNIVTAQAMYEG~~L~~WMSCV~~S~~QSTGQI
QCKVFDSL~~L~~NLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLE~~D~~DEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQBEFYDPMP~~T~~PNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTT~~S~~YPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FOR 523250

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

105101" 5623/2660

FIGURE 100

ACCCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCAACGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTGCGA

0972295.104504

SECRET

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCTGTCCC

FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCATCCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTGTCCCCGAA

0978295.101501

FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGAACC

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FIGURE 105

TCATAGGGGGGCGGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCTG

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"FOR" 5628260

FIGURE 106

TTCCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTTGGGGGCGCGATATTTCTTCTTGACAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTTCCTGCGAA

09978255.101504

FIGURE 108

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC
 CGCGTAGACCGACCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCCCCGTGCCCCG
 ACCGGTCCCCGCTTTTTTGTAAACCTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGT
 GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG
 CAGGTCTGAGCCTCGAGCCGAGCAGAGCTCAAATTCGAGGTCCCTTCACCGATGTTGT
 CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA
 CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT
 AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
 TATGGTTCAGTCTATGTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
 CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTGAATTGCCAGCAGAGAAT
 GATAAACCATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC
 ACCAATAGTGTCTAAGTCTCTGAGTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
 AAGAATGTAAGAGGCTGCAAGGTGAAGTTGAGAGGCTACGGGAGGAGAAACAAGCAGTTCAAG
 GAAGAAGATGGATGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGC
 CCCAACTGGGAAGGAAGAAGGCCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA
 TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
 GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
 AATGTATGATGACATCTCACAGGTCTTGCCCTTAAATTACCCCTCCCTGCACACACATACAC
 AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
 ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT
 GGCATATTGTAATGTCTATTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC
 TCTTAAATGACACCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT
 GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGGCCCACTCCCGGCCAGGCTG
 CTTTCCGTGCTTTCAGTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
 AGCCCAAAGGAATTGCACCTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
 TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
 GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAAATGCATA
 TTTAACTTATTTAATGTATTTTCATCTCATGTTTCTTATTGTGACAAGAGTACAGTTAATGC
 TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
 GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTTATTGGGATGCTGGAGAAGAGCTGCCA
 GGAAGTGTTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAAATTCTCAGTAGTG
 ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
 CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
 TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
 ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
 TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
 CTATGTAGCATCTTGAAGAAAAAATTATAATAAGCCCCAAATTAAGAAAA

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<subunit 1 of 1, 243 aa, 1 stop

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRDNVCFKVKTAPRRYCVRPNSGIID
AGASINVSVMQLPPFDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRVCVFE
LPAENDKPHDVEINKIIISTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLMRKTVQSNSPISALAPTGKEGLSTRLLALVVLFFIVGVIIGKIAL

Transmembrane domain:

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCCTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC
CCAAAATTAAGAATTCTTTTGTCAATTTGTACATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

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FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAACGTATTATTAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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SECRET

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNCGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

FIGURE 113

GGTGGCCCATTCCTGGCCAGGCTGCTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTTANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGT
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCAANTCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCAANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTCAATNTCATGTTTTCTTATTGTACAAAGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTTCOGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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CONFIDENTIAL

CCGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCCAGGCTGGAGTTCAGTGCCA
TGATCATGGTTTACTGTCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTACC
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAG
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGCCACCGACAGCAGGTTCAGCATCTTGGACAAA
AGGTTCTTAAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTATGATGGAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC
AGAGGATTGCCGAAGGGAGGCCCTTCCTTTCACTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACCTTGGAAATCAGCCCACGATCAAGAAAA
TGCCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGTCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAAGAGGAC
TACAACGTTGCTGTTGCGATCACTCCCCTAAAAATACGCCCAGATTTGCCCTCTGGATTACGG
GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT
GAACCTCTGTCAATAGCATTTC AACATTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAA
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTCACTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTTAGTTTAGTTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA
CAAAACTAATAACTGTTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTAAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACTAGTTTGAAGTATGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG
TAATTTTAGATATGTCCTTTCTTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGLTIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDSNLLYQYCDAESGSTGSGVYLRLLKDPDKKNWKRKIIAVYSG
HOWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

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FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCGGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTCCGGGCAACTCCTGGCACACTGCTCCTCTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCCGGGGAGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT
ATATCTGGAAACCAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTTCAATGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATAACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGAGGAGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAGPWSECSRTC GGGASYS LRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKCQ
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLV LKGPDLHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQEELEEGAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

05075022550

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGGTTCTGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCGG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG
GCGGCGGGTCACTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGGCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTTCAGCTCCAGCA
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTATATAGCCGGAGCAAAGTGGCTAACATTCTTTT
TACCAGGGAAGTAGCCCGCGCTTAGAAGGCACAAATGTACCGTCAATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACATTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGTGATGGGCTTTTTTCAAACTCCAGTAGAAGGTGCCCAGACTTCCATTTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAAGTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT
TGGGATAAGAGAATTTTCAAGCAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

0997885.104501

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLI NNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR
IVVSSKLYKYGDINFDDLNSEQSYNKSFCYSR SKLANILFTRELARRLEG TNVTNVNLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

09978295.101504
FIGURE 122

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

0973225.10154
105101-562B2560

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACCTTGGGTTTTTACTCCTGTAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAGAAATTGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACATATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCCCTCTT
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGGAGACTTCAAAGATGTATTAATTCTGGAAAACCTCAAGCAATTCC
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAACTTG
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAA

SECRET

<subunit 1 of 1, 406 aa, 1 stop

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTETISLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKEYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFVDVTYNWIQDKCVPPLVREI
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKCLKQFVFDLHSGKLHREFHGPDPPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Signal peptide:

Endoplasmic reticulum targeting sequence.

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

09078295.101501

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNGGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCCCTTTCCTAACCC
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTTCGTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

09978295-101501

FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTGCGGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAAATACCCCTGAATCCCCCTTGTA TCTCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG
GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGGCTTGTGGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTGACAGGTTTGAACCTGCACCTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTATTATAGGAACCTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC
ATGTGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCCTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

09973333.101501

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG
AATCCCCTTGTACTCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACACACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

09978295.101501

FIGURE 131

CGGACGCGTGGGGGAAACCCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTTCGTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAACTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAATTCCTCCTCATAGAGCTTTTAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAATAAAGTTACTCAAATCTGTG

099329.10501

QUESTIONS

<subunit 1 of 1, 323 aa, 1 stop

MAAPKGS LWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESEACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLFPLTLVRSFWSMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLMRNSQAHRNFLEDGESDGLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Signal peptide:

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCCG
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

09978295-101501

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGACCG
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

0597293-101501

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGGCCGCGGCTG
GGGATTCTTGTFTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTGAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACCTGTTTTAAGCCAC
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGACACAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACCTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACCAGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC
TCAGGAACCTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGGAAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGZEEQPPETAARCFQVSGYLDDCTCDVETIDRFNNYRLF
PRLQKLLESDFRYKVNLRPCPFWNDSQCGRDCAVKPCQSDEVPDGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAYVDLLLNP
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSKVLPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

105101 56232560

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTGAGGATGAGGNAAACAAAA
TGTTACTTTTGGAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

0907229.10511

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACCTCCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTTCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACCTATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCTGCCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTACAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPPNLDEHHPRLEFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

105101" 5622/550

FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACTTTATTTTATAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAATGGGAAATTCATCTCATCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

005707 56282560

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
ATTGAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
GATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTGCTCTGGAATAAGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
TGGTCTCCCGACACCTTGAAATAACCAATTACCCCGAGAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTCATAGGTTTGCAGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTAAGTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGAGAGGCCACTTTCACAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAAAAAA

097225 "101501
101501 "5023766

090310100

MQFTTMVLEEIIWTSLSFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSFVIAPGE
TVYYSVEYQGEYESLYTSHIWIPISSWCSLTEGPECDVTDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGFLHVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPVLALFAFVGFMILILV
VVPLFVWKMGRLLOYSCCPVVVLPTDLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAAGTGAAGTCTACCAAATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTCGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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FOR THE FUTURE

CCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGC
GCTGGTACTCTGGGCTGCAGTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCCCTCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTACAGCGTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTCT
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTT
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCAGTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCCCACAGGGCACTGAGGGGC
AACAGGGACCCCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCCATGGTGCCTGAGACTCCCCTTCGAGGATTGCACCCGCCCCTCCTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

03065-10

<subunit 1 of 1, 328 aa, 1 stop .

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLFLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLRDITITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSPPCSE
TWTWILIDRALNITSLQMHSRLRLSQNPSSQIFQSLSGNSRPLQPLAHRALRGNRDRHPRER
RCRGPNYRLHVDGVPHGR

Signal peptide:

Transmembrane domain:

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCGCGCGCCGAGCCTC
 GTTCGTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCTTGGCAGACTAACGAA
 GCAGCTCCCTTCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCCTGCCATTTCTCCAGGTTGAGGGAGC
 CGCAGAGGGCGAGGCTCGCGTATTCTGCAGTCAGCACCCACGTGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
 GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCGTCCGGTTTGGCT
 CACCTCTCCAGGAACTTCACACTGGAGAGCCAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
 ATCCTGAGGTCATTCAATATGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACACAGTGTCTTTCATGGCTAGA
 GCAATTCAGCCATGGTGGTTCCTCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATCGATGAGGATGGT
 GAGTGGTGGATAGCCAAACAACGAGGGGAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
 AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGCACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
 TTGGGAGCACACTGGGGAAGATATAGGCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGCGCCTGTATGTACACATTATACA
 CAGGTCTGTGGGCAACTAGTAACAGAAATCGGTTGTGCCATTAAATTTGTGTACATAACATGAACATCTGGGGGCG
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA
 CATGGGCGGCCCTGTTCTGCTTGGCCACCTAGTTTTTGGAGGGGGCTGTAGAGAAAATCTGTGTACAAAGAAGGG
 TCAGACAGGTATTATCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCCGACAAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCT
 TGTGAAGTAAGATTAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCAATTATGGT
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
 AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTCAAGTCTCTAAAGTAACAGTTCAGGCTGTG
 ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCTT
 CGTAACTGTATGCAAGCAAAATCCACATTATGCTCGTGTAAATGGAACCTCGAGTTTATTCTGATCTGTCCAGTATC
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCAGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
 AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAAATCCTCCAGGAGGAAAGGCATT
 AGAGTGTGCTGTGTTGTGAAACTGAATACTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCACTATTTTCAGCCCCAAAAGGTGCCAAATGCATA
 TAAATCTTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
 TTTTAGAAATCCTGTGTTAAATATTGCTATATTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
 GTTCTACGTTTCATATATTATATGGTGTCTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
 GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTPTTTC
 TGTAAATTTAGGCATATAGAAATATTAAATCTGATATTGCACCTCTTATTTTATATAAAATAATCCTTTAATATC
 CAAATGAATCTGTTAAATGTTTGAATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
 ATGAAAACATTCTAGTGATCATGTAGTAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
 AAATTGAGGTACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
 GAACAAAGATGAACTAATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGATATAA
 ATATTGCCATATCATGGTACCTATAATGGTGATATTTTGTCTATGAAAAATGTATTGTGCTTTGATACTAAA
 AATCTGTAAATGTTAGTTTTTGGTAATTTTTTCTGCTGGTGGATTACATATTAAATTTTTTCTGCTGGTGGTA
 TAAACATTAAATTAATCATGTTTCAAAAAA

09076295.101501

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDM
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYBHECNPYCPFRCSGPVCTHYTQVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLVLCNYSKGNWWGHAPYKHGRPCSA C PPSFGGGCRENLCYKEGSDRY
YPPREEETNEIERQQSQVHDTHVTRTSDDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKA FRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

105101" 56232660

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCACGCGG
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGGTGAAAAACCTCAGAAGGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAAAAGCTTCAAGTGGTACAACGCCCTGGAACGAGAAGCGCAGGGTCTACGAA
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCCGGA
GGAACAATGAGCTTGGTGGACACATTTTATTGCGAGTGTGCTCCATTCTAGCTTGGGAAGC
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAGAAGGTGTGGGGTCTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT
GACCATGCGCCCTTTCCTCTGTACATATACCTTAAGAACGCCCCCTCCACACACTGCCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAA

FIGURE 149

MSLLPRRAPPVSMRLAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

09978295.101501

FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTCAACCCGGTCTGCGTCATGTTAAACTCCAATGTCCTCCTGTG
 GTTAACTGCTCTTGCCATCAAGTTCAACCTCATTGACAGCCAAAGCACAGTATCCAGTTGTCAACACAAATTATGG
 CAAAATCCGGGGCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA
 TGCCTCACCCCCACTGGAGAGAGGGCGGTTTCAGCCCCCAGAACCCCGTCTCCTGGACTGGCATCCGAAATAC
 TACTCAGTTTGCTGCTGTGTGCCCCAGCACCTGGATGAGAGATCCTTACTGTCATGACATGCTGCCCATCTGGTT
 TACCGCCAATTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTTAAACATCTACGT
 GCCCACGGAAGATGGAGCCAAACAAAGAAAAACGAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA
 TATTATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA
 CATGATTGACGGCAGCATTTTGGCAAGCTACGGAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACT
 AGGGTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG
 GATTGAGGAGATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC
 CTGTGTCAGCCTGTTGACCTGTCCCCTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTCAGAGCGGCACCGC
 CCTGTCCAGCTGGGCAGTGAACACCAGCCGSCAAGTACACTCGGATATTGGCAGACAAGGTGCGGTGCAACAT
 GCTGGACACCACGGACATGGTAGAATGCCGTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC
 GGCCACCTACCATAGCCTTCGGGCGCGTGATCGACGGCGAGCTCATCCAGACGACCCCCAGATCCTGATGGA
 GCAAGGCGAGTTCTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCTGAAGTTGCTGGACGGCAT
 CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG
 CTACCCCTGAAGGGAAAGACACTTTGGCGGGAGACTTCAAGTTTATGTACACAGACTGGGCGGATAAGGAAAAACC
 GGAGACGCGCGGAAAAACCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCGTGGCCGCGACCT
 GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCTTCTATCATCACTGCCAAAGCGAAATGAAGCCCAGCTG
 GGCAGATTGGGCCCATGGTGATGAGGTCCCTATGTCTTCGCGATCCCCATGATCGGTCCCACCGAGCTCTTCAG
 TTGTAACTTTCCAAAGACGAGCTCATGCTCAGCGCGGTGGTTCATGACCTACTGGACGAACCTTCGCCAAAACCTGG
 TGATCCAAATCAACCACTTCTCAGGATACCAAGTTTCAATCAACAAAACCCAAACCGCTTTGAAGAAGTGGCCTG
 GTCCAAGTATAATCCCAAAGACAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC
 AACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCTCATTTGCACAACCTGAACGAGATATTCCAGTATGTTTCAAC
 AACCACAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCACC CGCGATCTCCCGCAAGATATGGCC
 AACCACAAACGCCAGCAATCACTCCTGCCAACATCCCAAACACTCTAAGGACCTCACAAAACAGGGCCTGA
 GGACACAACGTCTCTCATTTGAAACCAACGAGATTATCCACCGAATTAAGTGTCAACATTGCCGTGCGGGCGTC
 GCTCCTCTTCTCAACATCTTAGCTTTTGGCGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACTCACAG
 GCGCCCCAGTCCCCAGAGAAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT
 GAAGCAGCTGGAACACGATCACGAGTGTGAGTCTGTCAGGCACACGACACTGAGGCTCACCTGCCCGCCAGA
 CTACACCTCTACGCTGCGCGGTGCGCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA
 CACACTGACGGGGATGCAGCCTTTGCACACTTTTAAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
 CGGACATTTCCACCACTAGAGTATAGCTTTGCCCTATTTCCCTTCTATCCCTCTGCCCTACCCGCTCAGCAACAT
 AGAAGAGGGAAGGAAAGAGAGAAGGAAGAGAGAGAGAAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCCT
 GACTTAAGACAAAAATGCAAAAAGGCACTCATCCCATCCCGGCAGACCTTATCGTTGGTGTTTTCCAGTATTAC
 AAGATCAACTTCTGACCTGTGAAATGTGAGAAGTACACATTTCTGTTAAATAAAGTCTTTAAGATCTCTACCA
 CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTTCACACGTCATGGAAGCAGCT
 GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTAAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC
 CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGGCCAGCACATGAGCTGTAATCCAG
 AGAGAAGGAAACGTAGAAATTTATTATTAAGAAGTGGACTGTGCAGCGAAATCTGTACGGTTCTGTGCAAGAG
 GTGTTTGGCCAGCCTGAACATATATTTAAGAGACTTTGT

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FIGURE 151

MLNSNVLLWLTALAIAKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPPEPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTSLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVPIV
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKR DYSTELSVTI AVG
ASLLFLNILAFAALYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMI PNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCCTTACCCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG
GTGCCATGTTTCTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTGGTGATTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGAGTGCATTGAAGTGCCCGGAGTCCGCCCTGCC
CCGCGGCTACTACTTCCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCCTTGAAGTTGTTTGAAGTGCAGTGGAGAGAACCCCAAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTCTTCCCTCATCGTCTTTTTCTCCCTGGTGTTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCCTTTTTGTGACTGTCAACCCATGAGGTATGGAAGGAGCAGGCACTG
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAATCACAGAAC
AGAATTTATAGCCCAGGCTGCCGTGTTGTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG
AATCCACAAAGAAATTAATACTGGTAACACCACAGGCTTCTGACCATCCATTGTTGGGTT
TTGCATTTGACCCAACCTCTGCCTACCTGAGGAGCTTCTTTGGAAACCAGGATGGAAACT
TCTTCCCTGCCTTACCTTCCCTTCACTCCATTCAATTGTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTGATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT
TACGATTTTTTGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT
CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAATACACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

097295.10504

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPPQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLGMNAMVMTQYIRLTPDMQSKQ GALWNRVPCFLRDWELQVHFKIHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDK FVGLGVFVD TYPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRN LH YDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVFLPSVDNMKLP EMTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQE QSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

105701" 56282660

FIGURE 154

CCGAGCCGGGCGCGCAGCGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGGTGGGTCGTTAACTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAAT
 TGGGGTCTGGCTCAGAAATCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
 GACATGTTCCCGATTGAGGTGAAACCATGAAGAGAAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
 TGCTGCTGCTGGCCCTGCGCTGCTGGCCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
 CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTGACGGAGCCCCCTGTGA
 CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTATGCCCC
 CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTATTCCGCCACGGAGACAGGTACCCACTGTATGTCTATCCCA
 AAACAAAGCGACCAGAAATGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAACTGGAAGCTTTCA
 TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTGAAAGCCCTTGAACTCCTTGCCCTCTTACCCAAATCACC
 CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCGAAGCGGTGAGTGTGAGGGATA
 TCTATCTAAAGAAACACAACTCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA
 GCCGGACCCCTACAAAGTGGGCTGGCCTTGTCTTATGGCTTTCTCCAGATTTTGAAGGAAAGATTATTTCA
 GGCACCGACCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGTAAAGAACAGTATCTGGAAGAGGAGC
 AGCGTCGTGAGTACCTCTACGTTTGAAGAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG
 ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCAGCT
 TTCCCTGTACAGAAATGGCTGTGTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAAAGAAATTTGACTTCGGGTATTCTCTCTGGGTGCCACCCCATCTGAACCAACCATCG
 GCCGGATGCAGCGTGCACCGAGGGCAGGAAAGAGAGCTCTTGGCCCTCTACTCTGCTCATGATGTCACCTGT
 CACCACTTCTCAGTGCCTTGGGCTTTTCAAGCCAGGTTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
 GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGGATTCTTTACAATGGCGTCGATGTCACATTCCACACCT
 CTTTCTGCCAAGACCACCAAGCGTCTCTCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTAATGATGATGTCACAGGGAAGGATTCTAAAGG
 TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAGGTCCACTTCTAGTTTGTCTGTITAC
 TAAGGGTAGAAGATTATTGCTTTTAAAGGCTAAATATTGTTTGTGGGAACCAAGATGGTTGGGGTTGAACAGT
 AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTTACAGAGGAATAGAAGGTACTT
 TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
 TCTTCTGGCCCTGCCCATGTTACTATGTGATGGAACCAAGCACACCTCAACCAAAATTTTTTAATCTTAGACATT
 TTTACCTTGTCTTGTGAAGATTTCTGAAGTGATTTATCTAAAATAAAGGTTGGCAACCTTTTCTGTAAAGG
 GCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTATACTACTCAACTCTGT
 TTCTGAAGCAGGAAAGCCACACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA
 GATGGTGACAGACTTGGCCCTGGGCTGTAGTTTGTCTGACCCCTCATCTAAAATAAGGCTATACTACAATTGC
 ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAAATTAATCAATGGTTCTTCCAGTAACCTCTGCTAGAAACA
 CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTGTT
 CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT
 TTCTAAGACCAGTTTATAGTACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTGGTGGTTAGAAG
 GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAATTTATGGCTCATTCCCTTTGACAAGCTGTAGA
 ACTGGATTCAATTTTTAAACCATTTTCATCAGTTTCAATGGTAAATTCGATTGATTTTTAAATGGGTTTTTGA
 AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
 TGATTTCTGAACATAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCC
 AACTTTTTCTCTTTGTTTTGTCCAGTGTGCAATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

105401-56262660

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSPFC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLENLVRFVKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

09978295-101501
TDSFOT" 50282660

FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCCTTTTGAAGAACAGTACTGTGGA
 GCTATTAAAGAGATAAAAAAGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
 GCCGCTGTTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGACGCGCCTGAAGCACAAGCAGAT
 AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCACTGTCCCATTCTAT
 GGGCGAAGGAAGTCTCCTGACTTCACTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAAATGAT
 TCCTGCGCGACTGCACCGGAGTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGAAGTCTGTGGGAGACCGG
 ATGCACCCAGATACGCTATTTCAGTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT
 GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT
 GAATCCGCGCAGCGGAGCTTGGTACCGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
 TCAATTAAATCTAGACATTCTGATGGAGGATAAAGTGAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
 CGACAATGCGCCTTACTTTCTGTGAAGTGAATTAGAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT
 CCCTCTACCCACGCTGGGATCCGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
 CTTCTCCCTCATCGTGCAGAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGTGAAACGCGCCCTGGACCG
 CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGGCCTCCGACGGGGCGACCCGGTGGCGACAGGACCGCGCG
 CATCCGCGTATGGTTCTGGATGCGAACGACAACCGCACCAGCGTTTGTCTAGCCCGAGTACCGCGCGAGCGTTCC
 GGAGAAATCTGGCCTTGGGACGCGAGCTGTCTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT
 GAGGTATTCTTCGGTATGTGGACGACAAGGCGGCCAAGTTTCAAACTAGATTGTAATTTCAGGGACAATATC
 AACAAATAGGGGAGTTGGACCAAGAGGAGTCAAGATTCTACAGATGGAAGTGAAGCAATGGATAATGCAGGATA
 TTCTGCGCGAGCCAAAGTCTGATCACTGTCTGGAACGTAACGACAATGCCCGAAGTGGTCTCACCTCTCT
 CGCCAGCTCGGTTCCCGAAACTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAATGACCAAGATTCTGA
 GGAAACCGGACAGGTGATCTGTTTCAACAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA
 TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAACATCACAGTGACCGCCACTGACCG
 GGAACCCCGCCCTATCCACGGAACTCATATCTCGTGAACGTGGCAGACACCAACGACAACCCGCGGCTCTT
 CCCTCAGGCTCTTATTCGGCTTATATCCAGAGAACAAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA
 CGACCCGACTGTGAAGAGAACGCCAGATCACTTATCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC
 GTCTACGTGTCCATCAACTCCGACACTGGGTAAGTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA
 CTTGCAAGTGAAAGTGATGGCGCGGACACCGGGACCCGCCCTCAGCAGCAACGTGTGCTGTGAGCCTGTTCGT
 GCTGGACAGAACGACAATGCGCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCT
 GGCTCCCGCTCCGACAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGTGGACAGAGACTCCGGCCAGAAGCC
 CTGGCTGTCTACCGCTCTGCTCAAGGCCAGCGAGCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
 CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC
 CCCTCTCTCCGCCACTGTACGCTCACCGTGGCGGTGGCGGACAGCATCCCCAAGTCTGGCGGACCTCGGCAG
 CCTCGAGTCTCCAGCTAACTCTGAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG
 CGTCTTCTGGCCTTCGTCACTTGTCTGCTGGCGCTCAGGCTGCGGCGTGGCACAAGTCACGCTGCTGCAGGC
 TTCAGAGGGCGGCTTGACAGGAGCGCGCGTGCACATTTGTGGGCGTGGACGGGGTGCAGGCTTTCTGACAGAC
 CTATTTCCACAGAGTTTCCCTCACCAAGGACTCGCGGAAGAGTCACTGTATCTTCCCCAGCCCAACTATGCAGA
 CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGTGTGAGGTGATTGGTATTTTCTAAAGA
 CAGTCATGGGTTAATTGAGGTGAGTTTATATCAATCTTCTTTCTTTTCTTTTAAATGCTCTGTCTCCCAAGC
 TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAATCCTAGGCTCAAGCAATTATCCACCTTTGCGT
 CCGGTGTAAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCTATCTATCTATCTATCTATCTATCTATCTAT
 CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT
 CGAGGCGGGTGGATCACCTGAGGTGGGAGTTTGGAGCCAGCCTGACCAACATGGAGAAACCCGCTCTATACTAA
 AAAATACAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT
 TGCTTTAACTGGGAGGTGGAGGTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG
 AAATCTATCTCA

10576295.101501

0092E-101507

><subunit 1 of 1, 916 aa, 1 stop

MI PARLHRDYKGLLVLLGLILLGLTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLKRALDREEKAAHHLVLTASDGGDPVVRTGTARIRVMVLDANDNAPAFQAQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYISLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVLSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLALRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAFLQYTSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNCSVVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGS�TPVIPVLWEAEAGGSPEVGS�RPA

amino acids 1-30

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCA TGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTG TAGGTGGCAACTGGGTCTTT
ACAGCTGCCCACTGTAAAAAACGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTT CAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTCTTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT
CTGGTTC

1007858460

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

0007205-101501
"56232660"

RECEIVED

GGCGCCGGGTGCACCGCGGCGGGCTGAGCGCCTCTCGCGGCCGCGCGCCGCGCCCGCCCGC
CGCGCCGCCCAACGCCCAACCCCGGCGCGCCCTAGCCCCCGCGCGCGCCCGCCCGC
GCCCGCGCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCCCGGCCCGCCCGCCCGC
CCCCGGCGCGCGGGGAACCGGGCGGATTCTCGCGCGTCAAACACCTGATCCCATAAAC
ATTCATCCTCCCGCGCGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCGCGCCCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGCGCGGGCCGGGGCGCGGCGGTAGCGGCGGCGCCTGGG
TGCGGACCCCGGCCGCGGGGAGACGGGCGCCCCCGAAACGACTTTCAGTCCCCGACGCGC
CCCCCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCTGCGACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCCTGCCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCTGCCACATTCCACGGCCTGGGCGCCTACACACGCTGCACCTGGACCGC
TGCGGCCTGCAGGAGCTGGGCCCCGGGGCTGTTCCGCGGCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCTGCGACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTT
CCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCACGCCCACTTGGGCGCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGACCCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCCGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG
ACAGCCCGCCGGGCAACGGCTCTGGCCACGGCACATCAATGACTACCCCTTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGCTGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG
GTCTCTCCCTGATGGACGCCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGCGGCAGCGTTTGTTCCAGAACGCCGCCTCCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA
AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHGNRISHVPAASFACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDP
TFHGLGRLHTLHLDRCLQELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLNDNPWVCDRCRAPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLOGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSABPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

09070805 101501

SECRET

[illegible]

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLLESPFEFFQAELOV
IDINDHSPVFLDKQMLVKVSESSPPGTTFFPLKNAEDLDVGOQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREBEAEELRLTLTALDGGSPPRSGTAQVYIEVLVDNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPVETMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLKSAENFYTLTLTERPLDRESRAEYNITITVTDLGTPLITQ
LNMTVLIADVNDNAPAFQTSTYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA
ADLLTVYLVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site:

amino acids 418-421, 436-439, 567-570 and 786-789

03070225-101601

DONALDSON

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCGCGTAGCCGTGC
 GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT
 GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG
 AGTTTGCAGAGGAAAGTGGTGCCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
 GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
 AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
 TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTAGAGCCTAGCGGCGTCACCTGTGGTGCT
 GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
 AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
 CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
 GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTACAGGACCT
 TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT
 GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
 CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
 TGTTCTTAATATTTTATTTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
 GAACACTGGAAACACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAAT
 GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA
 CTGGTTGCTTGTATTTTCTTTATTTCTTTTAAATTAGTTTATTATGTATGCTACCATTCGAA
 CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
 GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
 CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA
 CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
 AAAAATATTCAATAG

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPVRVLRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEBYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLTLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

0097885-101501

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCCTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCACTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACATAA
AAATCATGAATATTTTAA

10978295.101504

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGP GSLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHS LCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSEKDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGLVITSVKRWQKGQREFKRISR SIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

10978265 101501

FIGURE 168

GTGGAGGCCGCGACGATGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCCTTGTGGCCAATGTGCT
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATAACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCCG
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG
TCCACCTGCCAGCAGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTTGGGGCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

SECRET

amino acids 468-471

FIGURE 170

GTCCCCATCCTGCTCAACTGGGTACGGTCCCTCTTAGACCAGCTCTGTCCATCATTTGCTGAAGTGGACCAAC
TAGTTCCTCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGCCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAGAAGCTCTAGTGGTT
TCTGAATCTAGCCCACTTGGCGGTAAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTAGGGGATTGTGACGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACCTGGGCGGAGGAGGCGGAGGCAAGCTGGGGCCGCTT
CCAGGTGTTGACGCTGCTCAGGCGCTCCCATTCAGGTGGACTCTGAGGAAGGCTTGTCTAGCAAGGCAGGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCTGGTTTCCCTTTGATGTGCTTGGCCAGGGGATT
GGCTGTGATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACAGCCAGGTTTCCCAAAGGCGAGCAGGA
GCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC
TAACACCTTGCACACCTACACTCTGTCTCCAGTGAGCACTTGGCTTGGATGTCAATGTGGGCCCTGATGAGAC
CAACATGCGAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTGATCTGGTGTAACTGC
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG
CCCTGCGTTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT
GACCGCCACAGACCTTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCTCCAGAGGT
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCGCAGGTCAATTCTGCGTCGACCTCTAGACTATGAAAAGAACC
TGCCTACGAGGTGGATGTTTCAAGCAAGGACCTGGGTCCAATCCTATCCAGCCCATTCGAAAGTTCTCATCAA
GGTCTGGATGTCAATGACAACATCCCAAGCATCCACGTCAATGGGCCCTCCAGCCATCACTGGTGTGAGAAGC
TCTTCCCAAGGACAGTTTTATTGCTCTTGTGATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG
CTGGCTGAGCCAGAGCTGGGGCACTTCAAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC
CACTGGACAGAGAGCAGTGGCCCAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAGAACAGCTCAGCATTGATCAGTGCATCAACGACAATGCACCTGTGTTTGAAGAAAGCAGGTATGA
AGTCTCCAGCGGGGAAAACAACCTTACCCTCTCTTCACTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT
TAATGGAAGAGTCTCATACCGCATCCAGGACTCCCGAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGGTCACTGAACATGAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG
GCAACCCATGCTTGCATCCAGTGTCTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCCTCCACAGGCCACCTGCTGGTGGC
CATCGAGACTCCCAATGGCTTGGGCCACGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT
CCTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCTCTACAGCATCCGCAATGG
AAATGAAGCCACCTCTTCATCTCAACCTCATACGGGGCAGCTGTTCCGTCAATGTACCAATGCCAGCAGCCT
CATTTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCATGTTTGTCAACAGTGTGGACCACTGAGGGACTCAGCCCGCAAGCCTGGGGCTTGGATGTGCGAT
GCTGACGGTGATCTGCCCTGGCTGTACTGTGCGGCATCTCGGGTTGATCTGGCTTTGTTCAATGTCCATCTGCCG
GACAGAAAAGAAGGACAAACAGGGCCTACAACCTGTGCGGAGGCGGAGTCCACTACCGCCAGCAGCCCAAGAGGCC
CCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCTGTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT
CGGGCAGTCCCAAGATGTGGACAAAGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCTGCAGGCCCCCTT
CCACCTCACCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACAGGGAGCACCGGCGGAGAGCCGAGAGGT
GCTGCAAGACAGCTCAACCTCTTTTCAACCATCCAGGCAGAGGAATGCCCTCCCGGAGAACCTGAACCTTCC
CGAGCCCGAGCCTCCACAGCCAGCCACGTTCCAGGCCCTTGAAGGTTGAGGACAGCCCAAGGGAGGCTGGC
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGCCTCTCTGCAACCTGAGACGGCAGCGACATCT
CAATGGCAAAGTGTCCCTGAGAAAGAAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC
TGCCTTCCCGGAGCGGAACCCCTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTAGCAAAATCTCCAGCTGCT
GTCCTTGTGCTCAGGGCCAATTCCAGCCCAAACCAACACCGAGGAATAAGTACTTGGCCAAGCCAGGAGG
CAGCAGGAGTGCAATCCCAAGACAGATGGCCCAAGTGCAAGGGCTGGAGGCCAGACAGACCAAGAACAGGAGGA
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCTGACCGGCCCTGGATGGCGAGACTCTTTTGGCCCTCAC
CACCAACTACCGTGACAATGTGATCTCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG
CAAGGCAGAGGCACAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCCGCTCCGAGGCGCTCCGGCGGCTCTCGGT
CTCGGGGAGGACCCCTCAGTTTAGACTTGGCCACCACTGCGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGTCCTGTGAACATACCTCAGACGCCCT
CTGGATCCAAGAACAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACTCACTAGCTAG
CGCGCGCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGACTAACAGCTGAC
TGACCAAGCAGCCCCCTTGAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT
TCTGTGCAAAACATATGTGGAGCACAAAGGTCAGTCTCTGGCAGAACAGATGCCAGGAGTATCACAGGCAGG
AAAGGTTGGCCTTCTTGGGTAGCAGGAGTCAGGGGCTGTACCTGGGGGTGCCAGGAATGCTCTCTGACCTAT
CAATAAGGAAAAGCAGTAAAAA

0973296 101501

100-443887-100

<MW: 129022, pI: 5.20, NX(S/T): 5

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTTCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTTTTCATGGTGCCTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
TCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCAATTGTCTCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAATCACTGAAGTCTTGGGAGAACTGCAGTTCAACTTCTATCACC GTTGGTT
TGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACCTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTCACTTCATAGCATACTCCTTCCCCGTGAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTGCGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAGGCGCGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTATTATGCAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAPFSCTMFELIIFEI
LGVLNSSSRYPFWKMNLCVILLILVFMVPPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIQVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALBELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

105101" 65234050

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCGGGTTNNGNATACCTTCCCAGAAAATATTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTC

09978295-101501

FIGURE 176

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT
TGGCTCCCTGCTCGTGAAGTCTCTTCTACGGGCTGTCGCTTCAATCTGGACGTGATGGGTGCTTGCAGAA
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCGAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTG
CCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACCGGGATATGATTGGTGGCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCAACCTGGACGACGG
TCCCTACGAGCGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCGGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGTCTGGTGCGTGAGAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAAACCA
CAAGGGTGTGTGGTCATCTGCGCAAGGACAGCGCCAGTCCGCTGGTGCCGAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGGTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAGATGGCTTTCCAGATATTGCACTGGTGGCTGCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCA
TGGGAGCAGCCTGGGGTTGTGCGCAAAACCTTCCAGGTGTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGTCTTTCAGGGCCAGACCCATCCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT
GGAGCAGCCCAACTGTGCTGGCGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT
TCCCGTGTGACGTTCTGTAGCCGTAACTGGAGAAACCCAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAGACAAGCTTCGGGCCATTGT
AGTGACCTGTCTACAGTCTCCAGACCCCTCGGTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCCTCAGTGGC
CCCCATCTCAATGCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCTGGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACC
TCTGCCCATGGATGTGGATGGAACAAAGCCCTGTGTTGCACTGAGTGGGCAGCCAGTCAATTGGCCCTGGAGCTGAT
GGTCAACCAACTGCCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCATGAAGCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGATGCTCTCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTCACTTCTACCTCAT
CCTTAGCACTCCGGGATCAGCATTGAGACCAGGAACTGGAGGTAGAGCTGCTGTGGCCACGATCAGTGAAGCA
GGAGCTGCATCCAGTCTCTGCAGAGCCCGTGTCTTTCAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
CCAGCAACTCTTCTCTCTGCTGTGGTGGTGGGGCGAGAGCCATGCACTGAGCGGGATGTGGGCAGCAAGGT
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTCCGCTCAGAACCTGGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGCGGGCGGGA
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGGAGCGGAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGC
TGAGAAGAAGAAAACATCACCTGGACTGCGCCGGGGCACGGCCAACTGTGTGGTGTTCAGCTGCCCACTCTA
CAGCTTTGACCGCGCGCTGTGCTGCATGTCTGGGGCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTATTGTCCGGGCCAATCATCAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA
TGCTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGCTGTGGTGGCAGAGAGGTGCCCTGGTGGGT
CATCTCTCTGGCTGACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCTCTGTGGAAGATGGGATTCTT
CAACCGGGCAAGCACCCGAGGCCACCGTGCCTCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCTGAGGAACAACCTGGGGCAGCCCCCGGGGGAGGGCCCCGATGCACA
CCCCATCTGGCTGTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCTAGGTTCC
CATGTCCAGCCTGGCTGTGGCTGCCCTCCATCCCTTCCCGAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCGATCAAGATTGGGAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC
TCTCCCAACCAACTTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGCTCTGATGCAAGGTGGGGAGAGGGATCCTAATCCCTTCTCTCCCATTCACCTGT
GTAAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCTTAACTAGAGGGTCCGGGAGGAGGTTGTGTCACTGA
CTCAGGCTGTCTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCTGCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTTATTAATAAATATTTGAGAACAATAAAAAAAAAAAAAAAAAA

00978295-101501

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFCBG
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFSGFSIDSGKGLVRAEELSFFVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSFGFGYSLAVADLNSDGWPDILVGAFFERQEELGGAVYVYLNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAVGAPFDGDGKVFYHGSLSGVVAKPSQVLE
GEAVGIKSFSGYSLSGSLDMDGNQYPDLLVGSGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRLVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEBPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPSQRAEIHFLKQCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPFVIGLELMVTNLPSDPAQPPQADGDDAHEAQLLVMLPDSLHYSQVRAIDPAEKPLCLSN
ENASHVECELGNNPMKRGAQVTFYLILSTSGISIEETTELEVELLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKEVTVSNQGQSLRTLGS AFLNIM
WPHEIANGKWLLYPMQVELEGGQGPQKGLCSRPNNILHLDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCLYSPDRAAVLHVWGRLLWNSTFLECY
SAVKSLEIVVRANITVKSSIKNMLRDASTVIVMVYLDPMVVAEGVPWWVILLAVLAGLL
VLALLVLLWKMGGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNWNGSPRREGP
DAHPIAADGHPGLGPDGHPGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-
407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408
and 1031-1047

105101-5522660

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAACAAGATGCTCAAGGTGTCAGCCGTAAGTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCCGGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC
TGGATGATAAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCAGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATGTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCAACCGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTTCGATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG
CATCTTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTGGACAGTGTGGTGTGTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGATGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAAATTATCTTCTTCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACCTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCTTACACAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTCACGAGAACAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGTGGGATCGTACATGTTAATTTTTTGAAGG
ATAATTCTAAGTGAAATTTAAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAA

09075305-10501
10501-5305-0907

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPI
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCEDGYYKPTQCHGSVGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDDDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

00078295-101501

FIGURE 180

CAGACTCCAGATTTCCCTGTCAACCCAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAAACAGTACCTGACGC
 CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGAATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC
 GCTCTGCCCTCCGGTGTCTGCTGCTGCTGGGGCGGCCGGCTTACACCTTCCCTCGATAGCGACTTACCTTTACCCCTT
 CCCGCCGGCCAGAAAGAGTGTCTTACCAGCCCATGCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTGA
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCCTCTCCAGAAGGCCAAACCTTAGTTTTTGAACAAAGAAAA
 TCAGATGGAGTTTCACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT
 TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAAGAGATTGGAAG
 AAATATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
 AGACTAAGCAAAAGTGGGCACATACAAATTTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAGAAAGC
 AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAAATTTAGTGGTTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAAACTAGAGTACGTAACATTGAAA
 AATGAGGCATAAAAAATGCAATAAACCTGTACAGTCAAGACCATTAAATGGTCTTCTCCAAATATTTTGAGATATA
 AAGTAGGAAACAGGTATAATTTTAAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
 TTGTACTTAAAGTGTGTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT
 TTTCTTAACTTTGAAAAATTTTGCAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC
 AGTCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGTAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT
 TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCA
 CTCTTCTCTATTTCATATGTCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTGTG
 AGATTTTTATAACCAATACATTTTCACTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
 CCAAGGCTGACATTTTACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
 AAATGAAGAATATAGTTTAAAGCTTCTCTCCATAGGACACATTTTCTCTAACCCCTTAACTAAAGTGTAGGA
 TTTTAAAAATTAATGTGAGGTAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
 TAATCATGTTATGTTAATTTTAAACATGATTGCTGACTGGATAAATCATTATTACCAGCAGTTATGAAGGAAATA
 TTGCTAAAAATGATCTGGGCCTACCATAAATAAATATCTCTTTTCTGAGCTCAAGAATTATCAGAAAACAGGAA
 AGAATTTAGAAAACTTGAGAAAACCTAATCCAAATAAATTTCACTTAAGTAGAACTATAAATAAATATCTAGA
 ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAAATTTCCAGTTAGCTGGAAG
 AAACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATCTGGTTTGAATTTATTTTGTAGCAGGTACATTTTATA
 AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTATTAAAAATTTTATTATAACAACCTTTTAT
 TAAATGGCCCTTTCTGAACACTTTATTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTAAA
 CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC
 TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAAATTTTAAAGTTATGCCCATTTATAACGTTGTTTAT
 GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT
 CTTGATGAGCAATAATGATAAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
 TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT
 ATGATCAATTACCTTAATTTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA
 AGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTGGCTGTTAAATTTGCAATGAGAAGCAAAATTTACA
 GTACCATAACTAATAAAGCAGGGTACAGATATAAATCTATGTCATCTTTCTATAAACTGTGATTAAGAAATCTA
 CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAAGTAACTTCTTACCATATAAAAACGATAATTGCTT
 TATTTGAAAAGAATTTAGGAATACTAAGGACAATTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
 CATAACCAAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTAAATTTTCTAAAGACATACTGTTTATCTGCTT
 CATATGCTTTTTTTAATTTCACTATTCATTCTTAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTT
 AACAGCTCATTTTGTCTTTTTCAATATACAAATTTTAAAAATACTACAATTTTAACTAAGGCCCAACCGATTTC
 CATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCTAGAGTTTGTCTGATATGCATTTGGATGATTAAAT
 GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGGTGTGTTGTAATTTTATGGTAAATTAATCCTTCTTA
 CACATAATGGTGTCTTAAATTTGACAAAAAATGAGCACTTACAATTTGTATGTCTCTCAATGAAGATTCTTTAT
 GTGAAATTTTAAAGACATTGATTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACATCAGTGTGTG
 CTCAAACTGCTTTTACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA
 AAATTTCAAGGAAAA

000713295-101501

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEY
QVLGDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKYITGTDIILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN
IQESNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

00073205-101501

FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTTCGAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCC
TTCITTTTCCTTTTTCTTCACCTTCATTTAGGCTTTTCTCTGTCTTCATGTCTTGAGATC
TCAGAGAATAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

00070295-101504

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM

DADLACQKRPSGKLVSVLSGARGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS

TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

00075295-101501

FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCAATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

109205.10501

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVDGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

00078295.101501

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGGCGCTCTCGGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCCTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCGAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCFATTTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

09078205-101501

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRITLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGLSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

09072205 101501
T0510T " 56222660

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

105101" 56282600

100-443887-100

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCCGCCGGTGTGGCTGCACCTACCAATCCCGTGCGCCGCGGCTGGGCCGTGCGAGAGTGCCTGTGCTTCTCTCCTGCACGCCGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTGTGGAATGAAAAGGAAGTATTAGAAATGAGCTGAAGACCATTCACAGATTAAATATTTTGGGACAGATTGTGATGCTTGATTCACCTCTGAAGTAAATGTAGACAGAAGTTCTCAAATTTGCATATTATCATCAACTGGAACACAGCAGTGAAATCTTAATGTTTCACTTAAATCAGAACTTGCATAAGAAAAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGGAGTGTCCAAAACCTGCAAGCAGTAGAGAAAATAGACAAGCTTTCAAGAAATTTGGCATTGAAGTTACATCTTGATAAAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGCCAGTATGAAGCTGGAATCTATTATCGTTATGATTTTGGTATTTGATGATGATCTCGAAATCATACATTGGAAAGAAGAGAAATTTGATGCTGTCTGTTAATCTCGGAGAACTGTGGTTTTGTAAATTTTTACTCCCCAGGCTGTTCACTGCCATGATTTAGCTCCCATATGGAGAGACTTTTGCTAAAGAAGTGGATGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAATGCTTTGGCGAATGAAAGGAGTCAACAGCTATCCAGCTCTTTCATTTTTCGGTCTGGAATGGCCCCAGTGAATA TCATGGAGACAGATCAAAGGAGATTTTAGTGAGTTTGTCAATGCAGCATGTTAGAAGTACAGTGCAGAACTTTG CAGGAAAATTTTGTCAAGTCCATACAACTGCTTTTGTCTGGTATTGGCTGGCTGATCACTTTTTTGTTCAAAAGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTCATTGGATGCTAAAGAAATATATTTGGAAGTAAATACATAATCTTCCAGATTTTGAACACTTTCCGCAACACACTAGAGGATCGTTTGGCTCATCATCGGTGGCTGTATTTTTTCATTTTGGAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACTAAAAACTCTACTTAAAAATGATCATATTCAGTTTGGCAGGTTTGACTGTCTCTGACCAGACATCTGTAGTAACTGTGATGTTTTTCAGCGCTCTCAGCAGTATTTAAAGGACAGAGCAACGAATTAAGAAATTCATCATGGAAAAGAGATTCTATATACATATCTTGCCTTTGCCAAAGAAAGTGTGAATTCATATTACACGCTTGGACCTCAAAA TTTTCTGCCAATGACAAAGAACCATGGCTGTGTGATTTCTTTGCCCTTGGTGTCCACCATGTCTGAGCTTTTACTACAGAGTTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAAGTTTGGTACACTAGATTGTACAGTTTATGAGGGACTCTGTAAACATGTATAACATTCAGGCTTATCCAACACAGCTGGTATTCAACAGATCCAACTATCATGAGTATGAAGGACATCACTCTGTGTGAACAAATCTTGGAGTTTCATAGAGGATCTTATGAATCTTCACTGGTCTCCCTTACACCCACCCTTCAACGCACTAGTTTACACAAAGAAACCAACGAAGCTGGAATGGTTGATTTTCTATTCTCCGTGTGTCTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAAGAAATGGCCCCGACATTAACTGGACTGATCAACGTGGGCAGTATAGATTGCCAACAGTATCATTCTTTTGTGCCAGGAAAACGTTCAAGATACCCCTGAGATAAGATTTTTTCCCCCAAAATCAAATAAAGCTTATCAGTATFCAGATTACAAATGGTTGGAATAGGGATGCTTATTCCTGAGAATCTGGGGCTAGGATTTTTTACTCAAGTATCCACAGATCAACACCTCAGACTTTCAGTGAAGAAAGTTTCAAGGGAAGAAATCATTTGGGTGATTGTTTCTATGCTCTCTGGTGTGGACCTTGCAGAAATTTGCTCCAGAAATTTAGACTCTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTCAAGCTTATGCTCAGACATGCCAGAAAGCTGGGATCAGGGCCTATCCAACTGTTAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAAGACAGATAAATACAGAGATGCBAAGCAATCGCTGCCTTAATAAGTGAAAAATTTGGAACCTCTCCGAAATCAAGGCAAGAGGAATAAGGATGAACCTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATCTGCACAGATGACATCAGAAGACACCTATTAGAATTTGATGATGGGAATGAATGAACATTATCTAGACTTGCAGTTGTACTGCCGAATTATCTACAGCACTGGTGTAAAGAAAGGGTCTGCAACTTTTTCTGTAAAGGGCCGGTTTTATAAATATTTTGACTTTGCAGGCTATAATATATGTTTCCACATGAGAACAAAGATAGAGTCATCATGTATTCTTTGTTATTGTCTTTTAAACAACCTTTAAAAAATATTAACAGTATCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCACTCCATGACCATTAGATGTCTGTCTCCCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTACAGTTTTTTGGCTGACCTGAAAAGAGGTAACTTAGTTTTTGGTCACTTGTCTCTTCTAAAGTGCATCCCTAACCATATTTTATATTTCGTTTTTAAAAACCCCATGATGTGGCACAGTAAACAAACCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTCTCA AAGGTTGAAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTCACACAGTAAGTACACAAATTTGAGCACAAGTAAGTGCACAAATCTGTAGTTTTCTGTATATCCAGGAAACCTGAGGGAAAAAATTA TAGCAATTAACCTGGGCATTGTAGAGTATCTCAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA TGTGTTTCATGTATTTTTGAAATTTGCTTTACATAGAAATTTTCCCACTGATAGTTGATTTTGGAGGCTCTAATATTTACATATTTGCTTCTGAACTTTGTTTTGACCTGTATCTCTTTATTTACATGTTTTGGTTTTTTTCACTCCTGTCCAGTCTATTTATTTTCAAATAGGAAAAATTACTTTACAGGTTGTTTTTACTGTAGCTTAT AATGATACGTAGTTATTCCAGTTACTAGTTTACTGTGCAGAGGGCTGCCTTTTTCAGATAAATATTGACATAATA ACTGAAGTATTTTTTATAAGAAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTTCTGTGTTGTTTGA CTCAAAGATACACAAATTTGTCAAGTACATGTAGTTGTTTGTATATAATTCAGAGTGTACAGAATGTTAAAAAT CCAATCAGTCAAAAGAGGTCAATGAATTTAAAGGCTTGCACCTTTTTTCAAAAAAAGAAAAA

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRD LKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLLEDNQGGQYESWNYYRYDFGI
YDDDP EIIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVN SYP SLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLVVFQP
SLAVFKGQGTKEYEIIHGGKILYDILAFAKESVNSHVTTLGPNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS
AEQILEFIEDLMNPSVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPTQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

097825-1050
105107-56282660

10333

AGACAGTAGTACCTCCTCCCTAGGACTACACAAGGACTGAACACAGAAGGAAGGACAGAGACAGACGAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAG
GTCGTTGGTGAAGTTTTTTCATTCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTTCTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTTCGAATCAATGCTGCAAAGCTTTATTTTACATTTTT
TCAGTCTTGATAATATTA AAAACATTGGTTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTCT
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTCAGCATTGAAAGATTTCCCTAGCCTCTTCCTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAA
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGPFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWPVLETDEVVRSLLD
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

00978295-101501

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGAGAGGGCCAGCCCGCCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTGGTGTTTATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT
CTAGGCCGCACACGGGGCCGCGCTGCCCACGCCCCGGCCGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCGACGCCCGCGCAGCCAGAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTCTGTCGCGACCCC
TTCGTGCGCCTGATCTCCGCCCTCCGCGAGCAAGTTGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTGCGCGTGCCCATGCTGCGGCTGTACGCCAACACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTGCGCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTAAGATTAATATATTTTCAAGTATTTAATACGA

09973295-101501

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTA
DSDVDEFLDKFLSAGVKQSDLPKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFFTKERAFDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLLRGAPYRDPLRIPREHVHNASAHLT FNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELNEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLD EDAQAQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLEGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

090709 5628/660

FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGGCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCAG
CCACTGGGCCCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCCTGGCCTCCGA
AGCCAACCTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGAATTTCTCTCATTT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCAACCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

097225.10150
FOR 56232660

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTG
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGGCCCTGGCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCG
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

105131-5628750

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCL
GCVNPFMTQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETI AVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

Y0510T.59294.000

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
 CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
 GCGCCCAACATGGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT
 CGCGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG
 TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
 TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAAAGAA
 TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTATTCAAGAACCAGGTTTGAGTG
 GCCGCTTCTTTGTCAACACTCTCCAGCATTCTTTTCATGCAAAGGATGGGATATTCCGCCGT
 TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
 AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGT
 TTTTATAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAAT
 CCTGCTTGGTGTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG
 TCTGGTCTTGGTGGTAATATGAAATGTTTCTATGTGCGCACTTCCAAGGCATTTATCTGAGC
 GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
 GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA
 GAAAGAAGATCTTGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTG
 CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCAGGAGAGGACGGTGTG
 ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGC
 TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC
 TGATAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG
 CCTGCAGTTTGTACCAAATCCTTAATTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCT
 CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
 GACAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
 CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCAGTCCTAATC
 AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
 CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTCTGTGTAAAGTATTTAT
 TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA
 ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
 TGCTATGTTTTATTTCTTACCTTTAATTTTTCCAGCATTTCACCATGGGCATTTCAGGCTCT
 CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
 TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
 GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
 TTACAAGACAGATTAATAAAAAAATGTTTTGTCCAAATATAGTTGTTGTTGATTTTTTTTT
 AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
 CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
 TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTCACTGATGTGCTTTTGGTGAAA
 GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC
 TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
 GCTAATTTCTTT

09078295-101501

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPBEAALPPEQSRVQPMASNWTLVMEGEWMLKIFYAP
WCPSCQQTDSWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKS PASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEDEEEDNLAAGVDEERSEANDQGPPGEDGV TRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 200

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAAACAATGGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTATAGTAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTACGTTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTATTTATTTATTTTTTTTGGATAGGGTCT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTTATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCTCACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTACTAAAAAGCAGGAACCTCTA
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTGTTGCCCAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTTGTATTTTTTTTAGT
AGAGACAGGGTTTTCTCCATGTGGTTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTTATGTTATGTGGATTTTCAT
TTCAATAAAAAAAACTCTTATCAAAAAA

0973295.101501

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

09378205-104501
T05T07-50282650

FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA
 CACAGGCTGGAGTGACAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC
 TCAGCCTCCCAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTCCGAGGAAAAATGACTCCCCAG
 TCCTGTCTGCAGACGACACTGTTCTCTGCTGAGTCTGCTTCTCTGGTCCAAGGTGCCACGGCAGGGGCCACAGG
 GAAGACTTTTCGCTTCTGCAGCCAGCGGAACAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG
 CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCTTTCCCTGCAGCCCCACCCTGCTTCCCGA
 TCCTTCCCTGACCCAGGGGCTCTACCACTTCTGCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC
 TATGGCAAGCGTGACTTCTTGTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG
 GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC
 GCCAGCTTACCTTCTCCTTCCACAGTCTCTCCACACAGGCCGCTCACAATGCCCTCGGTGGACATGTGCGAGCTC
 AAAAGGGACCTCCAGCTGCTCAGCCAGTTCTTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCTCC
 GCCAGCCAGCAGTTGCAGAGCCTGGAGTGAAGCTGACCTCTGTGAGATTCTAGGGGACATGGTGTCTCTTGGAG
 GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCACAGCCGGCTCCAGGACCTGCACATCCACTTCCCGG
 CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCCTCGAACACTCTTCCAGAGGACGAAAGGC
 CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGACAAGAAATTC
 AGCCAAGTCTCGGGTGAAGGCTTGGGGATTGTGTACAGAACACCAAAGTAGCCAACTCAGCGAGCCCGTG
 GTGCTCACTTTCAGCACCAGCTACAGCCGAAGATGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCCA
 TTGAGCAGCCCGGGCATTGGAGCAGTGCTGGGTGTGAGACCGTCAGGAGAGAAACCAAACATCCTGCTTCTGC
 AACCACTTGACCTACTTTCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGC
 CTCTCTCCTAGTGGGCTGTGTCTCTGCTGCCCTGGCTGCTTGTACCATTTGCCGCTACCTCTGCTCCAGG
 GTGCCCTGCCGTGCAGGAGGAACCTCGGGACTACACCATCAAGGTGCACATGAACCTGCTGCTGGCCGTCTTC
 CTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCC
 ATCTTCTGCACTTCTCCCTGCTCAGCTGCTTCTTCTGGATGGGCTCGAGGGGTACAACCTCTACCGACTCGTG
 GTGGAGGTCTTTGGCACTATGTCTCTGGCTTACCTTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCACTCTTT
 CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAATATGGCCCAATCATCTTGGCTGTGCATAGGACTCCAGAG
 GGCGTCATCTACCTTCCATGTCTGGATCCGGGACTCCCTGGTCACTACATCAACCACTGGGCTCTTCCAGC
 CTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCCGCTGCGCCCCACACCCAA
 AAGTGGTCACTGTGCTGACACTGCTGGGCTCAGCCTGGTCTTGGCCTGCCCTGGGCTTGTCTTCTTCTCC
 TTTGCTTCTGGCACCTTCCAGCTTGTCTCTGCTTACCTTTTCAAGCATCATCACTCTCTTCCAAGGCTTCCCTATC
 TTTCTCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCTCCCTCTGAAGAGCAACTCAGACAGCGCC
 AGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGATCTAGGCTCCAGCCCACTGCCCATGTGATGAAG
 CAGAGATGCCGCTCGTCCGACACTGCTGTGGCCCCGAGCCAGGCCAGGCCAGTCCAGCCGACAGCT
 TTGGAAGCCCAACGACCATGGAGAGATGGGCGTTGCCATGGTGGACGGAATCCCGGGCTGGGCTTTTGAATG
 GCCTTGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCTATGCTGCTAGGGTACTG
 TCCCCACATCTGTCCCAACCCAGCTGGAGGCTGGTCTCTCTTACAACCCCTGGGCCCAGCCCTCATTTCTGGG
 GGCCAGGCTTGGATCTTGGAGGTCTGGCACATCCTTAATCCTGTGCCCTGCTGGGACAGAAATGTGGCTCCA
 GTTGTCTGTCTCTCTGTGGTCACTTGGAGGCACTCTGCATCCTCTGTCAATTTAACTCAGGTGGCACCAGGG
 CGAATGGGGCCAGGGCAGACCTTCAGGGCCAGAGCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC
 AGCTCGCTACCTCTGAGCCAGGCCCTCCCTCCCTCAGCCCCCAGTCTCTCCCTCCATCTTCCCTGGGGTTC
 TCCTCTCTCCAGGGCTCCTTGTCTCTTCTGTTCAAGCTGGGGTCCCCGATTCCAATGCTGTTTTTTGGGA
 GTGGTTTCCAGGAGCTGCTGGTGTCTGCTGTAAATGTTTGTCTACTGCAACAAGCCTCGGCTGCCCTGAGCCA
 GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCTTTGTATGAGCTGCATTGCCCTTG
 CTCACCTGACCAAGCACAGCCTCAGAGGGGCCCTCAGCCTCTCTGAAGCCCTCTTGTGGCAAGAACTGTGGA
 CCATGCCAGTCCCGTCTGGTTTCCATCCCACACTCCAAGACTGAGACTGACCTCTCTGGTGAACCTGGCCCTA
 GAGCCTGACACTCTCTAAGAGGTTCTCTCAAGCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGT
 TAATTCTGTCCAACAAACACACAGGGTAGATTGTGCGCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTG
 GTCACCTCTCTGCCAACATTCAGTCTGGTATGTGAGGCGTGGTGAAGCAAGAACTCTGGAGCTACAGGGACA
 GGGAGCCATCATCTCTGCTGGGAATCCTGGAAGACTTCTGCAAGAGTCAAGCTTCAATCTTGACCTTGAAGAT
 GGAAGGATGTTCTTTTACGTAACCAATTCTTTTGTCTTTTGTATTTAAAAAGAGTACATGTTTATTGTAGAGA
 ATTTGAAACTGTAGAAGAGAAATCAAGAAGAAAAATAAAATCAGCTGTTGTAAATCGCCTAGCAAAAAA
 AA

0978295.101504

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFC SQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWS PQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDQLL
SQFLKHPQKASRRPSAAPASQQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLL VDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGC VVSALACLVTIAAYLCSRVP LPC
RRKPRDYTIKVHMNLLLA VFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLSYITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGF LIFIWYSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTTCTGTTCAACATGG

0972295-101501

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCAGGTTTTCCTTTGA
 TCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCCT
 GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCTTGGCGGTGGTGAAGAGAC
 TCGGGAGTCGCTGCTTCCAAAGTGCCCGCGTGAAGTGAAGCTCTCACCCAGTGCAGCCAAATGAGCCTCTTCGGGC
 TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC
 AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
 GAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
 AGGAAAATGTATGGATACAACCTTACGTTTGTATGAAAGATTGGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
 ATGATTTTGTAGAAGTTGAGGAACCCAGTGTGGAAGTATATTAGGGCGCTGGTGTGGTCTGGTACTGTACCAG
 GAAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTTCTGTAACAGGGT
 TCTGCATCCACTACAACATTGTTCATGCCACAATTCACAGAAGCTGTGAGTCTTTCAGTGTCTACCCCTTCAGCTT
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACAG
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAA
 GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT
 CAGTGTCCATAAGGGAAGAAGTAAAGAGAACCGATACCATTTTCTGCCAGGTTGTCTCCTGGTTAAACGCTGTG
 GTGGGAAGTGTGCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
 ACGAGGTCTTTCAGTTGAGACCAAGACCGGTGTGAGGGGATGACAAATCACTCACCGAGCTGGCCCTGGAGC
 ACCATGAGGAGTGTGACTGTGTGTGAGAGGGAGCAGGAGGATAGCCGCATCACACCAGCAGCTCTTGCCCA
 GAGCTGTGCACTGAGTGGCTGATTCTATTAGAGAAGCTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT
 TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCA
 ACAGCTCTTTTGAAGAGGAGGCTTAAAGGACAGGAGAAAAGGTTCTCAATCGTGGAAAGAAAATTAAATGTTGTAT
 TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTTCAGTTCTTTC
 GATACGGCTTAGGGTAATGTGCTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTTGCTTAAC
 TCTAAAGCTCCATGTCTGGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTCACAT
 ATGTAACCCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAAGTATGTGCTATGAATTTAACTTGT
 GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACA
 TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
 TTTTATTGTGTACATTTTTATATCTCCTTTTGACATTATACTGTGGCTTTTCTAATCTTGTAAATATATCT
 ATTTTTTACCAAAGGTATTTAATATCTTTTTTATGACAACCTTAGATCAACTATTTTGTAGCTTGGTAAATTTTTCT
 AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
 TTCTCGTATGGTCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA
 GACTTTTTGAAAAATAATTAAATATCATATCTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA
 AAGTAGACATTGAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
 AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGTGCTGTGCTGTGAGTAGGAACACATCTTATTTA
 TTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA
 GAAGTATGTCTCTTAACCAAGTTCACTTATTGTACTCTGGCAATTTAAAAGAAAATCAGTAAATATTTTGTCTGT
 AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGAATTTGAATCAAAAATGTATTGAATCATCAATATAAAGA
 ATGTGGCTATTTTGGGGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

05978295 "101501

FIGURE 207

MSLFGLLLLTALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCRCGSTGG

Signal sequence:

amino acids 1-14

09978295.101501

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGAAGA
 AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATCTTATCCTTTTAAACATAATCCTAATTTCC
 AAATCCTTGGGGCTAGATGGTTTCTAAAACCTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTCACAGAACACCCAGAACCTCACCCCTC
 ACCATTAACCACATACCAGACATCTCCCCAGCGTCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCA
 TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC
 TTTAGTGGACTCACTTATTTAAATCCCTTTTACCTGGATGGAACACAGCTACTAGAGATACCGCAGGGCCTCCCG
 CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
 AACATAGAAATCTCTACCTGGGCCAAAACCTGTTATATCGAAATCCTTGTATGTTTCATATTCAATAGAGAAA
 GATGCCTTCTTAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT
 TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC
 CTCAACCAATTACAAATCTTGACCTAAGTGGAAATTCCTCTGTTTATAATGCCCATTTCCCTGTGCGCCG
 TGTAAAAATAATTTCTCCCTACAGATCCCTGTAATGCTTTTGTGCGCTGACAGAATTAAAGTTTTACGTCTA
 CACAGTAACTCTCTTCAAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC
 CAAAACCTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCAATTTCTCCCGAGCCTCATCCAATTTGATCTG
 TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCAAGCATTTTCTTCACTGAAAAGCCTG
 AAAATCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTGCCATTACATAATCTTCAA
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTTAAAGAAATTTGCTAACCTCAGCATGTTTAAACAAATTTAAAGA
 CTGAAAGTCATAGATCTTTCAAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT
 GCCAGAACCTCTGTAGAAAGTTATGAACCCAGGTCTTGAACAAATTACATTATTTAGATATGATAAGTATGCA
 AGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGTACAAGTATGGGCAGACC
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTCAAGCATCTTTCTTCTCAAATGCCTG
 AATCTGTCAAGAAATCTCAATAGCCAAACCTTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTG
 GACTTCTCCAACACCGGCTTGATTTACTCCATTCAACAGCATTTTGAAGAGCTTCAAAAACCTGGAAGTTCTGGAT
 ATAAGCAGTAATAGCCATTATTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT
 CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTTCAAG
 AATCTGCTAAATTTAGAGGAATTAGACATCTTAAAAATTCCTAAGTTTCTTGCCTTCTGGAGTTTGTGATGGT
 ATGCCTCCAAATCTAAAGAATCTCTCTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
 CTAAGAACCTGGAACCTTTGGACCTCAGCCACAACCACTGACCCTGTCCCTGAGAGATTATCCAACCTGTTCC
 AGAAGCCTCAAGAATCTGATTTCTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC
 CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTCTC
 AACATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
 GTTAAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
 CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
 TCTGTATCTCTCTTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT
 TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGCTCAATATCACCAGACTGTTGCTATGATGCTTTTATTTGTGAT
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAGAGAGAAA
 CATTTTAAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA
 CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAAGATAGCATTTTAC
 TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG
 TCCAAGTTCTCCAGCTCCGAAAAGGCTCTGTGGGAGTTCTGTCTTGTAGTGGCCAAACAAACCCGCAAGCTCAC
 CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA
 ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAGGAGAGGCTGGC

097395-10501

FIGURE 209

MVFPMWTLKRQILILEFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTTNLTTLTINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSPLYLDGNQLEIPQGLPPLSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYYR
NPCYVSYSIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLNFLKCLNLSGNLISQTLNGSEFQPLAELRYLDIFSNNRLDLLH
STAFEEHLKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKLMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCAVWFVWVWNHTEVTIP
YLATDVTVCVGPGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLE
RDWLPQPVLLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHYPYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

090325.10501
10501.5628.660

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAACATGTTCCCTTC
 AGTCCTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTCTGTGAGTTATGCGCCGAAGAAATTTTCTA
 GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGACAGAGTGCAGCAATCGTCGACTACAGGAAG
 TTCCCAACCGGTGGGCAAAATATGTGACAGAACTAGACCTGTCTGATAATTTATCACACACATAACGAATGAAT
 CATTTCAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCAACCCCAATGTACAGCACCAGAACGGGAATC
 CCGGTATACAATCAATGGCTTGAATATCACAGACGGGCATTCTCAACCTAAAAAACCTAAGGGAGTTACTGC
 TTGAAGACAACAGTTACCCCAATACCCCTCTGGTTTGGCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA
 ATATATACAACATAACTAAAGAGGGCAATTCAGAGCTTATAAACTTGAAAAATCTCTATTTGGCCTGGAACGTCT
 ATTTTAAACAAAGTTTGGCAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT
 CACTATCTTTCAATTTCTTTTACACGTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA
 CCCAGATCAAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACTATTACTAGATTAAAGCGGGAAT
 GTCCGAGGTGCTTCAATGCCCATTTCCATGCGTGCCTTGTGATGGTGGTGTCTCAATTAATATAGATCGTTTGT
 CTTTTCAAACTTGACCAACTTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAAATGCTGCCTGGT
 TTAATAATATGCTCATCTGAAGGTGCTGATCTTGAATCTCAACTATTATTAGTGGGAGAAATAGTCTCTGGGGCAT
 TTTTAAACGATGCTGCCCGCTTAGAAATCTTGACTTGTCTTTAACTATATAAAGGGGAGTTATCCACAGCATA
 TTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAAC
 TCRAGAAGATGATTTCCAGCCCCGTGATGAGCTTCCAACTTATCGACTATCAACTTGGGTATTAATTTTATTA
 AGCAATTCGATTTCAAACTTTTCCAAATTTCTCCAATCTGGAATTTATTTACTTGTGAGAAACAGAAATATCAC
 CGTTGGTAAAGATACCCGGCAGAGTTATGCAAAATAGTTCCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAA
 CAGATTTTGAAGTTTGACCCACATTGCAACTTTTATCATTTTCAACCGTCTTTAATAAAGCCCAATGTGCTGCTT
 ATGGAAGAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCAATTGGGCCAAACCAATTTGAAATCTTCTCTGACA
 TTGCTGTCTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGGAACTGAATTTTCAAGCCATTCCTCATG
 TCAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGTCTTACTGAATGTCCGACTTGG
 AAGTTCTAGATCTCAGCTATAATTCACACTATTTGAGAACTAGCAGGCGTAACACATCATCTAGAAATTTTCAAA
 ATTTCACAAAATCTAAAGTTTAAACTTGAGCCACAACAACATTATATCTTTAACAGATAAGTATAACCTGGAAA
 GCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTATA
 TCTCCATTTTCAAAGGTCTCAAGAATCTGACAGCTCTGGATTATCCCTTAATAGGCTGAAGCAGATCCCAAATG
 AAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACATACATAAATGATAATATGTTAAAGTTTTTAACTGGA
 CATTACTCCAGCAGTTTCTCGTCTCGAGTGTCTGACTTACGTGGAACAAACTACTCTTTTAACTGATAGCC
 TATCTGACTTTACATCTTCCCTTCGGACACTGCTGTGAGTCTAAGCAGGATTTCCACCTACCTCTGGCTTTC
 TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG
 AAATAAGACCACCACCAATTTATCTATGTTGGAATACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAG
 ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTTCCAGACTGGTAGATGTCAATTTGTGCCAGTCTGT
 GGGATCAAGAGGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTTCAGATGTCACTGCAGTGATATTAT
 TTTTCTTCAAGTTCTTTTATCACCACCATGGTTATGTTGGCTTGGCTGCCCTCACCATTGTGTTTACTGGGATGTTT
 GGTATATATAATGTGTGTTTAGCTAAGGTAAAGGCTACAGGTCTCTTTCCACATCCCAAACCTTCTATGATG
 CTTACATTTCTTATGACACCAAGATGCCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACTTGAAG
 AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC
 TCATGCAGAGCATCAACCAAGCAAGAAAACAGTATTTGTTTAAACCAAAAAATATGCAAAAAGCTGGAACCTTTA
 AAACAGCTTTTACTTGGCTTTGACAGGCTAATGGATGAGAACATGGATGTGATTATATTTATCCTGCTGGAGC
 CAGTGTACAGCATTCTCAGTATTTGAGGCTACCGCAGCGGATCTGTAAGAGCTCCATCTCCAGTGGCCTGACA
 ACCCGAAGGCAGAAGGCTTGTTTTGGCAAACTCTGAGAAATGTGGTCTTGAAGTGAATGATTACGGTATAACA
 ATATGTATGTGATTCATTAAAGCAATACTAACTGACGTTAAGTCATGATTTGCGCCATAATAAAGATGCAAG
 GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTTATCCAAACCTTAGTGGTTTAAACAACACA
 TTTGCTGGCCACAGTTTGTGAGGGTCAGGAGTCCAGGCCAGCATAACTGGTCTCTGCTCAGGTTGTCTCAG
 AGGCTGCAATGTAGGTGTTTACCAGAGACATAGGCATCACTGGGCTCACACTCATGTGGTTGTTTCTGGAATTC
 ATTCCTCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCAAGGCAGCTTGTCTC
 ATCAGAGCTAGCAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGAATCGAATCAAAAAGTGAT
 ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCAGGTCCCACCAAGCTCCATGGGAGTGACCACC
 TCAGTCCAGGGAAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCAGTTGGTTCATCAACTATTTTCCCT
 TGACTGCTGTCTGGGATGGCTGCTATCTTGTATGATAGATTGTAATATCAGGAGGCAGGGATCACTGTGGACC
 ATCTTAGCAGTTGACCTAACACATCTTCTTTTCAATATCTAAGAACTTTTGGCACTGTGACTAATGGTCTTAATA
 TTAAGCTGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCTGTTTAT
 TTACAGTTGCTTTTACAAATATTTGCTGTAACTTTGACTTCTAAGGTTTAGATGCCATTTAAGAAGCTGAGATGG
 ATAGCTTTTAAAGCATCTTTTACTTCTTACCAATTTTAAAGGTATGCAGCTAAATTCGAAGCTTTTGGTCTATA
 TTGTTAATTTGCCATTGCTGTAAATCTTAAATGAATGAATAAAATGTTTCATTTTACAAAAA

09072295 101501

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNNGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFQNLTLQLRYLNLSSTSLRKINAAWFKNM
PHLKVLDLEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNLEI IYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELEV
LDLSYN SHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTTELHINDNMLKFFNWT
LLQQFPRLLELLDLRGNKLLFLTDSLSDFTSSLRLLLLSHNRISHLPSGFLSEVSSLKHLDL
SNLLKTINKSALETKTTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTFFYDAYISYDTKDASVTDWVINELELYHLEESRDKNVLLCLEERDWDPLAII
NMQSINQSKKTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLEFWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

009895-10404

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGTAGGAGGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCATCCTTCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCTTCCTG
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTCTTCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA
AAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTATGACGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAACQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

00978205-101501

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGCCCCGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCT
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCC
TGCAGCGTGTGTACCAGCCCTTCCTCACACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTCCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA
CTCGTGA¹CTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCTCCTCCCTTCTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAAATAAAAATGAAACGTG

FIGURE 215

MRGSEQVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

097895-101501
TOSTOT 5622/660

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGGGAGGGGACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGAGGAGCAGCT
GGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCCTTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCAGCACATAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

09978295-101501
105101-5628260

FIGURE 218

GGTTGCCACAGCTGGTTTATAGGGCCCCGACCACTGGGGCCCCCTTGTCTAGGAGGAGACAGCCTCCCGGCCCGGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCGCTCAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGTGGGCCGGTTTATCGGGAGG
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGAGCAGGAATTCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAACTCCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCCGCTCATGATGGCCCCGGCAAAAGGGCATTTTCTACCTGACCCCTTTTCTCATCTCTGGGGACATGTACAC
TCTTCTTCCGCTTTGAGTGCCGCTACCTGGCTGTTTCTGCTCTCTCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCTGGAGTGATTCTCTGGGGCGCTACCAGATG
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCGAGGGCCAGCGACCACCGCTTCGTA
TCAAGAATTTCCAGATAAAACAACAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCTCCCC
GGGCCTCCCATTTGAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGAATTTGTG
TTGGAAGAGGAACTACCGCTACTTCTACCTCTTCTATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTGGCCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAAGT
TTCTAGAACTCCTCATTTGCTTCTTTACACTCTGGTCCGTCTGGGACTGACTGGATTTCATACTTTCTCTGTG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGGGCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA
TTTTGGCACTGGAGGAAAGTGGAAAGTCGACCTCCAGTACTCAAGAGACAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCCACAGAACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTT
TAATTAGGGCTATGAGAGATTTAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTTCTTTGGTCTTTAGTCAACCCAGTTGCCACTGGCATTCTTCTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAGATGTCAGTCACTCTGATAACTGGAATAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCCCTGGACCCCCCTCTCTTCCCTCCAGATCCAGCCCTCCTGCTTGGGGTCA
TGGTCTCATTTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTGACTCCTGCTCCCATAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCAATTTCTTTTCTCAGAGGAAGCCGAGTGCTCACTTAAAC
ACTATCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAGTTCTTCCATTAAGCCT
CGGCTGAGTGAGGGAAAGCCAGCACTGCTGCCCTCTCGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCAGAGCCACTT
CACCTTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTCAGGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACTTTTCTATTTTGAAGGCGATTAACTGTGTCTAATGCA

0973295.101504

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGNCV GKRNRYFYFYL
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLI CFFTLWSVVGLTG FHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLD RRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPPEPPQEAAEA EK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTGGCTTTGGACTCTCNCTTTCT
CCACAGAGCNCCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

09978295.101501

FIGURE 221

GTGTTGTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGGCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTTTC
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTACGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAACTATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGGTGGCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

09073305-101501

FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTNYPPISEAKGTGVFVGQKGTLOCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHNTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLLKF

Signal peptide:

amino acids 1-28

00978295-101501

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

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FIGURE 224

ATGGCTGGTGAACGGCGGGGCGGGGACGGGGCCGCGGCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCACAGCACCTGCCTTACA
GAGGCTGTCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAAGCCATACTGAAGCACCTGCTTGAAAAACACACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTACCGTCTACATCAGTGGCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACAGCTCTGGGCTCTTCTGCCCCCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCGCTCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTCCCCAGGACAGCGGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCCGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTT
CTGTCTTTCTTGTCTGTCACCATTTGGAGTTGAGTGAATCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG
TCCTGTGTGCGGAGGTGGCAGACCTGCATCTCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGGACCGCAAGCAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAACATGTTGAATTGTACAACCTTCTCTGCCAAGGTATGGCTGACCAGCTCCGCAAG
CCTCCAGCCGAGACCACTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC
GTCTTCCCCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACCTCGGTGGCATC
GGTGTGGTCATGGGCCATGAGTTGACGATGCCCTTGTATGACCAAGGGCGGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACCGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACCGGCCCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCAGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTTGCGG
CACTTCCGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGTCTTGGGTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCTCCTCAATCACCACATTG
TGCCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTTCCGTGTACCCCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

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FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVLTAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFERALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPQQLCEVW

Type II Transmembrane domain:

amino acids 32-57

COPIES OF THE

[illegible]

FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCAC TGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCCGA
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCTTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCCT
CCTTTCTTTCTTCTTTTCTTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCCTTCTCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTTCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAGAGATTGCATTTGAGCCAGGTCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGAACCAACCCCAAGGCCCTGAACCTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCGGTGTACCCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCTATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACCTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTTCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

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FIGURE 229

CCCACGCGTCCGAGCCGCCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA
 GGAGGGGAGGCAAAAACACCGAAAAACAAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG
 GGGGAAGAAAGAAAAGAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG
 TGGGGGAGTGCAGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG
 CTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG
 CTGCCTGCTACCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCCTGGGCGGCCGTGG
 ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT
 TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTCGCGGAGGTGATAAGTGGTCAGT
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAGGGACTACAGCCTCCAGATACAGAATG
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTTTCAGACTCAACATACACCCAGAACA
 ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACCAGAGCCTTCCA
 TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT
 TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCAGGAAAATGCTGTGTCTATT
 CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTAGGAAATTAAT
 CTGGCACCGTGACCCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT
 CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT
 TCAAAATTTTAGCACAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA
 ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCCCT
 CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT
 TGTGTTGACACTGTCTCTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA
 TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT
 GGTACAGTTTGTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
 TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTGTATTAGCTACATTA
 CCTTGTGAAGCAGTACACATTGCTCTTTTAAAGACGTGAAAGCTCTGAAATTACTTTTAG
 AGGATATTAATTGTGATTTTATGTTTGTAACTTACAACTTTTCAAAGCATTTCAGTCATGGT
 CTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAATATTGCAGTGAATATGTGATTCTTTAA
 GGCTGCAATACAAGCATTGAGTTCCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG
 CATTTTTTTCTTTTTTGATAAAAAGCAAATAATATTGCCCTCAGATTATTTCTTCAAATA
 TAACACATATCTAGATTTTTCTGCTTGCATGATATTGAGTTTTCAGGAATGAGCCTTGTAA
 ATAAGTGGCTGTGCAGCTCTGCTTCTCTTCCCTGTAAGTTGAGCATGGGTGTGCCTTCATAC
 AATAATATTTTCTCTTGTCTCCAATAATAAATGTTTGTCTAAATCTTACAATTTGA
 AAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACTATCTCTAAGTAACGAAGGAGC
 TATTGGACTGTAAAAATCTCTTCCCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT
 AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTCT
 TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAATGACAGCACA
 GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTCACTAGTCCAAGCCAAAAA
 TTTTAAGATGATTTGTGAGAAAGGGCACAAGTCTTATCACCTAATATTACAAGAGTTGGTA
 AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC
 AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA
 CAAGGAATAATTTCTGATCCAGGATCGTCCCTTCAAATGGCTGTATTTATAAAGGTTTTTGG
 AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATGACCTGCCA
 AGGTAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA
 AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 230

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGDTAVLR CYLED
GASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKR DYSLQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFPDVRKV KVVVNFAPT IQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL
NPPSTAQYGITGSADVL FSCWYLVLT LSSFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACCAAATTGCAATGGAGCCTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTCTGAATCTGCAGGC
GCGGCTCCGGGTCCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCTTGCAAGGCCCACTCACCTGGGTCCGCGTCAAGCATGAGCACTGCTGCAGCGGGT
AGACAACTTCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCAACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCGGGACCACTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAAGGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCCAAAGGGGAACTGGAATAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGGGGCCTCCTGGAGCCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTTTCTTGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCCCTCCTGGTGCAGTGGGACACCAGGTGC
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCAAGTGTGCGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGACCCCGAAACCTTTCA
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

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FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLIILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQVRDNFTQNPGMFRIKGEQAGPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPGSGPQGPVGKGEAGLQGPQAGPKQATGTPGPQGEKSGKGDGGLIGPKGETGTKGE
KGDGLGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPAGKGDQGPGLQGVPG
PPGAVGHGPAKGEPPGSGSPGRAGLPGSPGSPGATGLKGSKGDGTLQGGQGRKGESGVPGPA
GVKGEQGSPLAGPKGAPQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLQVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGGCCAAACTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTTCG
TGATTCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTTC
CCACAACTGCACCTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

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FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1, stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

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FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG
 TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCCGCGCTGGCTGTG
 CGCTGGGGCGCTGGTGTCTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGGGTGGTTTA
 TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
 AGGAACAGAACAAAACCTTTAGCTTGCAAAGCAAATTCATCCCAGTGGAAGAATTTGGCC
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTTACCCAAATAAGACTCATCCC
 AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAACC
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACTTTTCACTGCTTTCTCTCCTC
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAAGTGAAGACTTCTTTAA
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATGTAAATTGCCAGATATGGGAAAGT
 TTTAGAGGAAATAAGGTTAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
 CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCTCCT
 GGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATGTCAGAGGCTGTTGGTCTTCCAA
 GTATTCCTGTTTATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC
 TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
 CTTTACTGGAACTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
 CGAGAATTTACAATGTGATAGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT
 TGTTTATGAAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAGACCTAGAAGAA
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA
 GAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
 ACTAAAAAAGTCCCTTCCCAGAGTTTCACTGGCATGCCCAGGATAAGCAAATTTGGGATCTGG
 AAATGATTTTGAAGTGTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA
 AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT
 GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTCCG
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTCGAGATTATG
 CTGTAGTTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT
 TGCTTCCAAGTTCACTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA
 TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTATTTGATCCATTAGGGTTACCAGAC
 AGGCCTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC
 ATTCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCCTCCAAGGCCT
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT
 TTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGT
 TGAATATTATATATAA

097365-1051
 1051-097365

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIIINEDGNEIFNTSLFEPPPPPGYENVSDIVPPFSAFSPQGMPEGLVYVNYARTEDFF
KLERDMKINCSGKIVIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNGAGDPLTPGYPANAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHISTNEVTRIYNVIGTLRGAVEPDRYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYES
WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDSLFSVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHKNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713